Clone name	SEQ ID NO	Enantioselectivity for Neryl Butyrate (N) or Geranyl Butyrate (G)
1f15(G2)	21	G
3C12	22	G
3N19(G2)	23	G
G2.2	24	G
2C3	25	G
2F11	26	G
KV11(6C7)	27	N
KV6(3A1)	28	N
KV2(2D1)	29	N
N2.5	30	N
KV5(2H6)	31	N
3E5	32	G
G2.1	33	G
3H24(G2)	34	G
KV10(4G6)	35	N
KV12(6D4)	36	N
N2.2	37	N
N2.3	38	N
N2.1	39	N
KV4(2E12)	40	N
KV9(4C6)	41	N
7D6	42	G
3F3	43	G
2D11(G2)	44	G
3C23(G2)	45	G
G2.3	46	G
2A3	47	G
2F4	48	G
2B9(G2)	49	G
2C5	50	G
KV1(2A6)	51	N
2D13(G2)	52	G
3C8	53	G
2D5	54	G

FIGURE 1

Clone Name	E value for Neryl Butyrate	E value for Geranyl Butyrate
Exemplar (sgc2 and sgd2)	---	2.1
Exemplar (2h6)	1.4	---
Exemplar (14g14)	1.8	---
Exemplar (3f19a11)	2.2	(not tested)
Exemplar (3e5)	---	3.0
Exemplar (3n19)	---	3.8

FIGURE 2

```
                                        1                                                                      75
SEQ:001-405(pumilus)  (1) ------ATGAAATTTGTAAAAAGAAGGATCATTGCA------CTTGTAACAATTTTGGTGCTG-TCAGTCACATCGC
SEQ:002-406(subtilis) (1) ------ATGAAATTTGTAAAAAGAAGAAGGATCATTGCA------CTTGTAACAATTTTGATGCTG-TCTGTTACATCGC
SEQ:003-402(megat.)   (1) ------ATGAAATTTGTAAAAAGAAGAAGGATCATTGCA------CTTGTAACAATTTTGGTGCTG-TCAGTCACATCGC
SEQ:004-400(lentus)   (1) ------ATGAAATTTGTAAAAAGAAGAAGGATCATTGCA------CTTGTAACAATTTTGGTGCTG-TCAGTCACATCGC
SEQ:005-396(circul.)  (1) ------ATGAAATTTATAAAAAGAAGAAGGATCATTGCA------CTTGTAACAATTTTGGTGCTG-TCAGTCACATCGC
SEQ:006-392(azotof.)  (1) ------ATGAAATTTGTAAAAAGAAGAAGGATCATTGCA------CTTGTAACAATTTTGGTGCTG-TCAGTCACATCGC
SEQ:007-398(firmus)   (1) ------ATGAAATTTGTAAAAAGAAGAAGGATCATTGCA------CTTGTAACAATTTTGGTGCTG-TCAGTCACATCGC
SEQ:008-393(badius)   (1) ------ATGAAATTTGTAAAAAGAAGAAGGATCATTGCA------CTTGTAACAATTTTGGTGCTG-TCAGTCACATCGC
SEQ:009-Dc5h          (1) ------ATGAAATTTGTAAAAAGAAGAAGGATCATTGCA------CTTGTAACAATTTTGATGCTG-TCTGTTACATCGC
SEQ:010-Dc5f          (1) ------ATGAAATTTGTAAAAAGAAGAAGGATCATTGCA------CTTGTAACAATTTTGATGCTG-TCTGTTACATCGC
SEQ:011-Dc5c1         (1) ATGAAAGTGATTTTGTTAAGAAAAGGAGT-TTGCAAATTCTTGTGCCCTGCTTGCTGGTCAGGTCAATAGC
SEQ:012-Dc5a2         (1) ATGAAAGTGATTTTGTTAAGAAAAGGAGT-TTGCAAATTCTTGTGCTTGCTTGCATTGGTGATGGGTTCAATGGC
SEQ:013-Dc512         (1) ATGAAAGTGATTTTGTTAAGAAAAGGAGT-TTGCAAATTCTCATTGCGCTTGCATTGGTGATTGGTTCAATGGC
SEQ:014-Sga           (1) ------ATGAAATTTGTAAAAAGAAGAAGGATCATTGCA------CTTGTAACAATTTTGATGCTG-TCTGTTACATCGC
SEQ:015-Sgc           (1) ------ATGAAATTTGTAAAAAGAAGAAGGATCATTGCA------CTTGTAACAATTTTGATGCTG-TCTGTTACATCGC
SEQ:016-Sgd           (1) ------ATGAAATTTGTAAAAAGAAGAAGGATCATTGCA------CTTGTAACAATTTTGATGCTG-TCTGTTACATCGC
SEQ:017-Sgf           (1) ------ATGAAATTTGTAAAAAGAAGAAGGATCATTGCA------CTTGTAACAATTTTGATGCTG-TCTGTTACATCGC
SEQ:018-Sgh           (1) ------ATGAAATTTGTAAAAAGAAGAAGGATCCTTGCA------CTTGTAACAATTTTGATGCTG-TCTGTTACATCGC
SEQ:019-Mt2b1         (1) ATGAAAGTGATTTTGTTAAGAAAAGGAGT-TTGCAAATTCTTGTGCCCTTGTGCCTTAGTGATAGGTTCAATGGC
SEQ:020-H2a           (1) ------ATGAAATTTGTAAAAAGAAGAAGGATCATTGCA------CTTGTAACAATTTTGATGCTG-TCTGTTACATCGC
```

Figure 3a

(Signal peptide coding region) → ┆ (Mature coding region)

```
                         76                                        150
SEQ:001-405(pumilus) (65) TGTTTGCGATGCAGCCGTCAGCAAAAGCCGCT|GAACACCAATCCAGTTGTTATGGTTCAC-GGTATCGGAGGAGCT
SEQ:002-406(subtilis) (65) TGTTTGCGTTGCAGCCGTCAGCAAAAGCCGCT|GAACACCAATCCAGTCGTTATGGTTCAC-GGTATTGGAGGGGCA
SEQ:003-402(megat.)  (65) TGTTTGCGATGCAGCCGTCAGCAAAAGCCGCT|GA-CACAACCAGTTGTTATGGTTCACTGGTATCGGAGGAGCT
SEQ:004-400(lentus)  (65) TGTTTGCGATGCAGCCGTCAGCAAAAGCCGCT|GAACACCAATCCAGTTGTTATGGTTCAC-GGTATCGGAGGAGCT
SEQ:005-396(circul.) (65) TGTTTGCGATGCAGCCGTCAGCAAAAGCCGCT|GAACACCAATCCAGTTGTTATGGTTCAC-GGTATCGGAGGAGCT
SEQ:006-392(azotof.) (65) TGTTTGCGATGCAGCCGTCAGCAAAAGCCGCT|GAACACCAATCCAGTTGTTATGGTTCAC-GGTATCGGAGGAGCT
SEQ:007-398(firmus)  (65) TGTTTGCGATGCAGCCGTCAGCAAAAGCCGCT|GAACACCAATCCAGTTGTTATGGTTCAC-GGTATCGGAGGAGCT
SEQ:008-393(badius)  (65) TGTTTGCGATGCAGCCGTCAGCAAAAGCCGCT|GAACACCAATCCAGTTGTTATGGTTCAC-GGTATCGGAGGAGCT
SEQ:009-Dc5h         (65) TGTTTGCGTTGCAACCGTCAGCAAAAGCCGCT|GAACACCAATCCAGTCGTTATGGTTCAC-GGTATTGGAGGGGCA
SEQ:010-Dc5f         (65) TGTTTGCGTTGCAACCGTCAGCAAAAGCCGCT|GAACACCAATCCAGTCGTTATGGTTCAC-GGTATTGGAGGGGCA
SEQ:011-Dc5c1        (75) CTTCATCCAGCCGAAAGAAGCCAAA-GCGGCT|GAGCATAATCCGGTTGTAATGGTGCAT-GGCATGGGCGGTGCG
SEQ:012-Dc5a2        (75) CTTCATCCAGCCAAAAGAGATCAGA-GCGGCT|GAGCATAATCCGGTTGTGATGGTACAT-GGCATGGGCGGTGCG
SEQ:013-Dc512        (75) GTTTATCCAGCCGAAAGAGGCGAAG-GCGGCT|GAGCATAATCCGGTTGTGATGGTGCAT-GGCATTGCGGTGCC
SEQ:014-Sga          (65) TGTTTGCGTTGCAACCGTCAGCAAAAGCCGCT|GAACACCAATCCAGTCGTTATGGTTCAC-GGTATTGGAGGGGCA
SEQ:015-Sgc          (65) TGTTTGCGTTGCAACCGTCAGCAAAAGCCGCT|GAACACCAATCCAGTCGTTATGGTTCAC-GGTATTGGAGGGGCA
SEQ:016-Sgd          (65) TGTTTGCGTTGCAACCGTCAGCAAAAGCCGCT|GAACACCAATCCAGTCGTTATGGTTCAC-GGTATTGGAGGGGCA
SEQ:017-Sgf          (65) TGTTTGCGTTGCAACCGTCAGCAAAAGCCGCT|GAACACCAATCCAGTCGTTATGGTTCAC-GGTATTGGAGGGGCA
SEQ:018-Sgh          (65) TGTTTGCGTTGCAACCGTCAGCAAAAGCCGCT|GAGCACCAATCCAGTCGTTATGGTTCAC-GGTATTGGAGGGGCA
SEQ:019-Mt2b1        (75) CTTCATCCAGCCAAAAGAAATCAAA-GCAGCT|GAGCACCAATCCAGTCGTTGTGATGGTACAT-GGTATTGGAGGAGCG
SEQ:020-H2a          (65) TGTTTGCGTTGCAACCGTCAGCAAAAGCCGCT|GAACACCAATCCAGTCGTTATGGTTCAC-GGTATTGGAGGGGCA
```

Figure 3b

```
                              151                                                                        225
SEQ:001-405(pumilus)  (139)  TCATACAATTTTGCGGGAATTAAGAGCTATCTCGTATCTCCAGGGCTGGTCACGGGGCAAGCTGTATGCGGTTGAT
SEQ:002-406(subtilis) (139)  TCATTCAATTTTGCGGGAATTAAGAGCTATCTCGTATCTCCAGGGCTGCGTCGCGGGACAAGCTGTATGCAGTTGAT
SEQ:003-402(megat.)   (139)  TCATACAATTTTGCGGGAATTAAGAGCTATCTCGTATCTCCAGGGCTGGTCACGGGGCAAGCTGTATGCGGTTGAT
SEQ:004-400(lentus)   (139)  TCATACAATTTTGCGGGAATTAAGAGCTATCTCGTATCTCCAGGGCTGGTCACGGGGCAAGCTGTATGCGGTTGAT
SEQ:005-396(circul.)  (139)  TCATACAATTTTGCGGGAATTAAGAGCTATCTCGTATCTCCAGGGCTGGTCACGGGGCAAGCTGTATGCGGTTGAT
SEQ:006-392(azotof.)  (139)  TCATACAATTTTGCGGGAATTAAGAGCTATCTCGTATCTCCAGGGCTGGTCACGGGCGAGCTGTATGCGGTTGAT
SEQ:007-398(firmus)   (139)  TCATACAATTTTGCGGGAATTAAGAGCTATCTCGTATCTCCAGGGCTGGTCACGGGCCAAGCTGTATGCGGTTGAT
SEQ:008-393(badius)   (139)  TCATACAATTTTGCGGGAATTAAGAGCTATCTCGTATCTCCAGGGCTGGTCACGGGGCAAGCTGTATGCGGTTGAT
SEQ:009-Dc5h          (139)  TCATTCAATTTTGCGGGAATTAAGAGCTATCTCGTATCTCCAGGGCTGCGTCGCGGGACAAGCTGTATGCAGTTGAT
SEQ:010-Dc5f          (139)  TCATTCAATTTTGCGGGAATTAAGAGCTATCTCGTATCTCCAGGGCTGCGTCGCGGGACAAGCTGTATGCAGTTGAT
SEQ:011-Dc5c1         (148)  TCTTATAACTTTGCTTCGATCAAACGATACTTAGTATCACAGGGATCACAAGGATCAAAACCAACTTTTGCAATCGAT
SEQ:012-Dc5a2         (148)  TCTTATAACTTTTGCTTCGATTAAAAGTTACTTGGTATCACAAGGATGGATCGAAACCAATTATTGCTATCGAT
SEQ:013-Dc512         (148)  TCTTATAACTTTTTTCTATTAAAAGTTATTTGGCCACACAGCTATCTCGTATCGAAACCAATTATATGCTATTGAT
SEQ:014-Sga           (139)  TCATTCAATTTTGCGGGAATTAAGAGCTATCTCGTATCTCCAGGGCTGCGTCGCGGGACAAGCTGTATGCAGTTGAT
SEQ:015-Sgc           (139)  TCATTCAATTTTGCGGGAATTAAGAGCTATCTCGTATCTCCAGGGCTGCGTCGCGGGACAAGCTGTATGCAGTTGAT
SEQ:016-Sgd           (139)  TCATTCAATTTTGCGGGAATTAAGAGCTATCTCGTATCTCCAGGGCTGCGTCGCGGGACAAGCTGTATGCAGTTGAT
SEQ:017-Sgf           (139)  TCATTCAATTTTGCGGGAATTAAGAGCTATCTCGTATCTCCAGGGCTGCGTCGCGGGACAAGCTGTATGCAGTTGAT
SEQ:018-Sgh           (139)  TCATTCAATTTTGCGGGAATTAAGAGCTATCTCGTATCTCCAGGGCTGCGTCGCGGGACAAGCTGTATGCAGTTGAT
SEQ:019-Mt2b1         (148)  TCTTATAACTTTGCTTCGATTAAAAGTTATTTGGTTAACCAAGGCTATCTCTTAACCAATTATTTGCTATCGAT
SEQ:020-H2a           (139)  TCATTCAATTTTGCGGGAATTAAGAGCTATCTCGTATCTCCAGGGCTGGTCGCGCGGGACAAGCTGTATGCAGTTGAT
```

Figure 3c

```
                                          226                                                                              300
SEQ:001-405(pumilus)  (214)  TTTTGGGACAAGACAGGGACGACGAATTATAAACAATGGCCCGGTATTATCACGATTTGTGCAAAAGGTTTTAGACGAA
SEQ:002-406(subtilis) (214)  TTTTGGGACAAGACAGGGACGACGCACAAATTATAAACAATGGACCGGTATTATCACCACGATTTGTGCAAAAGGTTTTAGATGAA
SEQ:003-402(megat.)   (214)  TTTTGGGACAAGACAGGGACGACGAATTATAAACAATGGCCCGGTATTATCACGATTTGTGCAAAAGGTTTTAGACGAA
SEQ:004-400(lentus)   (214)  TTTTGGGACAAGACAGGGACGACGAATTATAAACAATGGCCCGGTATTATCACGATTTGTGCAAAAGGTTTTAGACGAA
SEQ:005-396(circul.)  (214)  TTTTGGGACAAGACAGGGACGACGAATTATAAACAATGGCCCGGTATTATCACGATTTGTGCAAAAGGTTTTAGACGAA
SEQ:006-392(azotof.)  (214)  TTTTGGGACAAGACAGGGACGACGAATTATAAACAATGGCCCGGTATTATCACGATTTGTGCAAAAGGTTTTAGACGAA
SEQ:007-398(firmus)   (214)  TTTTGGGACAAGACAGGGACGACGAATTATAAACAATGGCCCGGTATTATCACGATTTGTGCAAAAGGTTTTAGACGAA
SEQ:008-393(badius)   (214)  TTTTGGGACAAGACAGGGACGACGCACAAATTATAAACAATGGCCCGGTATTATCACGATTTGTGCAAAAGGTTTTAGACGAA
SEQ:009-Dc5h          (214)  TTCAAGGACAAGACAGGGACGACGCACAAATTATAACAATGGCCCGGTATTATCACGATTTGTGCAAAAGGTTTTAGACGAA
SEQ:010-Dc5f          (214)  TTCTAAGGACAAAACAGGGAATAACCGCAACAATAACCAATGGTCCGCGTCTATCGAGATTCGTCAAAGATGTGTTAGACCAAA
SEQ:011-Dc5c1         (223)  TTCATAGGACAAAACAGGGCAATAACCTAAACAATAACCGCAACAATGGTCCGCGTCTGAGGCTCTCGAGATTCGTGAAAGACGTACTAGCCAAA
SEQ:012-Dc5a2         (223)  TTCATAGGACAAAACAGTAATAACCGCAACAATAACCGCAACAATGGTCCGCGTCTATCCAGATTCGTCAAAGATGTGCTAGCCAAA
SEQ:013-Dc512         (223)  TTCATAGGACAAAACAGGGCAATAACCGCAACAATAACCGCAACAATGGTCCGCGTCTATCCGCGTCTATCGAGATTCGTCAAAGATGTGTTAGACAAA
SEQ:014-Sga           (214)  TTCAGGGACAAGACAGGGACAATAACTTAAAACAACGGTCCAGTATTATCGCGTTTCAGTATTATCGCGTTTGTGAAAAAGGTATTAGATGAA
SEQ:015-Sgc           (214)  TTCTGGGATAAGACAGGGCAATAACTTAAAACAACGGTCCAGTATTATCGCGTTTGTGAAAAAGGTATTAGATGAA
SEQ:016-Sgd           (214)  TTTAGTGACAAAACAGGGCAATAACTTAAAACAACGGTCCAGTATTATCGCGTTTGTGAAAAAGGTATTAGATGAA
SEQ:017-Sgf           (214)  TTCAAAGACAAGACAGGGGAATAACCGCAACAATGGTCCGCGTCTATCGAGATTCGTCAAAGATGTGTTAGACAAA
SEQ:018-Sgh           (214)  TTCATTGACAAGACAGGGGAAATAACCGCAACAATGGTCCGCGTCTATCGAGATTCGTCAAAGATGTGTTAGACAAA
SEQ:019-Mt2b1         (223)  TTCATAGACAAAACAGGGAATAACCGCAACAATGGTCCGCGTCCTCGTTTATCTAGATTCGTCAAAGATGTGCTAGACAAA
SEQ:020-H2a           (214)  TTCAGGGACAAGACAGGGACGAATAACCGCAACAATGGTCCGCGTCTATCTAAATTCGTCAAAGATGTGTTAGACAAA
```

```
                             301                                                                            375
SEQ:001-405(pumilus)  (289)  ACGGGTGCGAAAAAAGTGGATATTGTCGCTCACAGTATGGGTGGCGCGAACACACCTTACTACATAAAAAATCTG
SEQ:002-406(subtilis) (289)  ACGGGTGCGAAAAAAGTGGATATTGTCGCTCACAGCATGGGGGCGCGAACACACTTTACTACATAAAAAATCTG
SEQ:003-402(megat.)   (289)  ACGGGTGCGAAAAAAGTGGATATTGTCGCTCACAGCATGGGTGGCGCGAACACACTTTACTACATAAAAAATCTG
SEQ:004-400(lentus)   (289)  ACGGGTGCGAAAAAAGTGGATATTGTCGCTCACAGCATGGGTGGCGCGAACACACTTTACTACATAAAAAATCTG
SEQ:005-396(circul.)  (289)  ACGGGTGCGAAAAAAGTGGATATTGTCGCTCACAGCATGGGTGGCGCGAACACACTTTACTACATAAAAAATCTG
SEQ:006-392(azotof.)  (289)  ACGGGTGCGAAAAAAGTGGATATTGTCGCTCACAGCATGGGTGGCGCGAACACACTTTACTACATAAAAAATCTG
SEQ:007-398(firmus)   (289)  ACGGGTGCGAAAAAAGTGGATATTGTCGCTCACAGCATGGGTGGCGCGAACACACTTTACTACATAAAAAATCTG
SEQ:008-393(badius)   (289)  ACGGGTGCGAAAAAAGTGGATATTGTCGCTCACAGCATGGGGGCGCGAACACACTTTACTACATAAAAAATCTG
SEQ:009-Dc5h          (289)  ACGGGTGCGAAAAAAGTGGATATTGTCGCTCACAGCATGGGTGGCGCGAACACACTTTACTACATAAAAAATCTG
SEQ:010-Dc5f          (289)  ACGGGTGCCAAAAAAGTAGATATTGTGGCTCATAGTATGGGTGGAGCGAACACGCTATACTATATCAAGAATCTA
SEQ:011-Dc5c1         (298)  ACGGGCGCCAAAAAAGTAGATATTGTGGCTCATAGTATGGGTGGAGCGAACACGCTATACTATATTAAAAACCTA
SEQ:012-Dc5a2         (298)  ACAGGTGCCAAAAAAGTTGATATTGTGGCTCATAGTATGGGTGGAGCGAACACGTTATACTATATTAAGAATCTA
SEQ:013-Dc512         (298)  ACGGGTGCCAAAAAAGTAGATATTGTGGCTCATAGTATGGGTGGAGCGAACACGCTATACTATATCAAGAATCTA
SEQ:014-Sga           (289)  ACCGGTGCGAAAAAAGTGGATATTGTCGCTCACAGCATGGGTGGCGCGCTAACACGCTTTACTACATAAAAAATTTG
SEQ:015-Sgc           (289)  ACCGGTGCGAAAAAAGTGGATATTGTCGCTCACAGCATGGGTGGCGCGCTAACACGCTTTACTACATAAAAAATTTG
SEQ:016-Sgd           (289)  ACCGGTGCGAAAAAAGTGGATATTGTCGCTCACAGCATGGGTGGCGCGCTAACACGCTTTACTACATAAAAAATTTG
SEQ:017-Sgf           (289)  ACAGGAGCCAAAAAAGTAGATATTGTGGCTCATAGTATGGGTGGAGCGAACACATTATACTATATTAAGAATCTA
SEQ:018-Sgh           (289)  ACAGGAGCCAAAAAAGTAGATATTGTGGCTCATAGTATGGGTGGAGCGAACACACGCTATATTATTAAGAATCTA
SEQ:019-Mt2b1         (298)  ACGGGTGCCAAAAAAGTAGATATTGTGGCTCATAGTATGGGTGGCGCGAACACGCTATACTATATTAAGAATCTA
SEQ:020-H2a           (289)  ACGGGTGCCAAAAAAGTAGATATTGTGGCTCATAGTATGGGTGGCGCGAACACGCTATACTATATTAAGAATCTA
```

Figure 3e

```
                                          376                                                        450
SEQ:001-405(pumilus) (364) GACGGCGGAAATAAAATTGAAAAACGTCGTAACGCTTGGCGGCGCGAACCGTTCGACGACGAAGGCGCTTCCG
SEQ:002-406(subtilis) (364) GACGGCGGAAATAAAAGTTGCAAAACGTCGTGACGCTTGGCGGCGCGAACCGTTTGACGACGAAGGCGCTTCCG
SEQ:003-402(megat.)   (364) GACGGCGGAAATAAAATTGAAAAACGTCGTGACGCTTGGCGGCGCGAACCGTTTGACGACGAAGGCGCTTCCG
SEQ:004-400(lentus)  (364) GACGGCGGAAATAAAATTGAAAAACGTCGTAACGCTTGGCGGCGCGAACCGTTTGACGACGAAGGCGCTTCCG
SEQ:005-396(circul.) (364) GACGGCGGAAATAAAATTGAAAAACGTCGTAACGCTTGGCGGCGCGAACCGTTTGACGACGAAGGCGCTTCCG
SEQ:006-392(azotof.) (364) GACGGCGGAAATAAAATTGAAAAACGTCGTAACGCTTGGCGGCGCGAACCGTTTGACGACGAAGGCGCTTCCG
SEQ:007-398(firmus)  (364) GACGGCGGAAATAAAATTGAAAAACGTCGTAACGCTTGGCGGCGCGAACCGTTTGACGACGAAGGCGCTTCCG
SEQ:008-393(badius)  (364) GACGGCGGAAATAAAATTGAAAAACGTCGTAACGCTTGGCGGCGCGAACCGTTTGACGACGAAGGCGCTTCCG
SEQ:009-Dc5h        (364) GACGGCGGAAATAAAAGTTGAGAAACGTCGTCACAATTGGTGGAGCAAACGACTCGTTCAAGCAGGCAAGGCGCTTCCG
SEQ:010-Dc5f        (364) GATGGCGGCGATAAAATTGAAAACGTCGTCACAATTGGTGGAGCAAACGACTCGTTCAAGCAGAGCATTACCA
SEQ:011-Dc5c1       (373) GACGGTGGAGATAAAATTGAAAACGTCGTCACAATTAGGTGGAGCAAACGACTCGTTCAAGCAGAGCATTACCA
SEQ:012-Dc5a2       (373) GACGGCGGCGATAAAATAGAAAACGTTGTACACTTGGTGGAGCGAACGACTCGTTCACTCAGAGCATTACCA
SEQ:013-Dc512       (373) GATGGCGGCGATAAAATTGAGAACGTTGTCACAATTGGTGGAGCAAACGACTCGTTCCACTCAGAGCATTACCA
SEQ:014-Sga         (364) GATGGCGGTAATAAAATTGAAAACGTCGTAACACTTGGCGCGCGGAATCGTTCTTGACAGGCAAGGCGCTTCCG
SEQ:015-Sgc         (364) GATGGCGGTAATAAAATTGAAAACGTCGTAACACTTGGCGCGCGGAATCGTTCTTGTGACAGGCAAGGCGCTTCCG
SEQ:016-Sgd         (364) GATGGCGGTAATAAAATTGAAAACGTCGTAACACTTGGCGCGCGGAATCGTTCTTGTGACAGGCAAGGCGCTTCCG
SEQ:017-Sgf         (364) GATGGTGGCGATAAAATTGAGAAATTGTCACAATTGGTGGAGCAAACGACTCGTTCAAGCAGAGCATTACCA
SEQ:018-Sgh         (364) GATGGTGGCGATAAAATTGAAAACGTCGTCACAATTGGTGGAGCAAACGACTCGTTCAAGCAGAGCATTACCA
SEQ:019-Mt2b1       (373) GATGGCGGCGATAAAATTGAAAACGTCGTCACCATTGGTGGAGCAAACGACTCGTTCACTCAGAGCATTACCA
SEQ:020-H2a         (364) GATGGCGGCGATAAAATTGAGAACGTTGTCACAATTGGCGGAGCAAACGACTCGTTCGAGCAGAGCATTACCA
```

Figure 3f

```
                              451                                                        525
SEQ:001-405(pumilus)  (439)   GGAACAGATCCAAATCAAAAGATTTTATACACATCCATTTACA-GCAGTGCCGATATGATGATTGTCATGAATTACTT
SEQ:002-406(subtilis) (439)   GGAACAGATCCAAATCAAAAGATTTTATACACATCCATTTACA-GCAGTGCCGATATGATGATTGTCATAAATTACTT
SEQ:003-402(megat.)   (439)   GGAACAGATCCAAATCAAAAGATTTTATACACATCCATTTACA-GCAGTGCCGATATGATGATTGTCATGAATTACTT
SEQ:004-400(lentus)   (439)   GGAACAGATCCAAATCAAAAGATTTTATACACATCCATTTACA-GCAGTGCCGATATGATGATTGTCATGAATTACTT
SEQ:005-396(circul.)  (439)   GGAACAGATCCAAATCAAAAGATTTTATACACATCCATTTACA-GCAGTGCCGATATGATGATTGTCATGAATTACTT
SEQ:006-392(azotof.)  (439)   GGAACAGATCCAAATCAAAAGATTTTATACACATCCATTTACA-GCAGTGCCAATATGATGATTGTCATGAATTACTT
SEQ:007-398(firmus)   (439)   GGAACAGATCCAAATCAAAAGATTTTATACACATCCATTTACA-GCAGTGCCGATATGATGATTGTCATGAATTACTT
SEQ:008-393(badius)   (439)   GGAACAGATCCAAATCAAAAGATTTTATACACATCCATTTACA-GCAGTGCCGATATGATGATTGTCATGAATTACTT
SEQ:009-Dc5h          (439)   GGAACAGATCCAAATCAAAAGATTTTATACACATCCATTTACA-GCAGTGCCGATATGATGATTGTCATGAATTATTT
SEQ:010-Dc5f          (439)   GGCACAGATCCAAATCAAAAATTCTTTACACATCCGTCTATA-GCTCAGCGAGATCTTATTGTCGTCAACAGCCT
SEQ:011-Dc5c1         (448)   GGCACCGATCCAAATCAAAAATTCTTTACACATCCGTCTATA-GCTCAGCCGATCTCATTGTCGTCAACAGCCT
SEQ:012-Dc5a2         (448)   GGCACAGATCCAAATCAAAAATTCTTTACACATCCGTCTATA-GCTCAGCCGATCTTATCGTCGTCAACAGCCT
SEQ:013-Dc512         (448)   GGCACAGATCCAAATCAAAAATTCTTTACACATCCGTCTATA-GCTCAGCCGATCTTATTGTCGTCAACAGCCT
SEQ:014-Sga           (439)   GGTACTGATCCCAACCAAAGATCTTGTACACATCCGTTTACA-GTAGTGCTGATATGATTGTTATGAATTACTT
SEQ:015-Sgc           (439)   GGTACTGATCCCAACCAAAGATATTGTACACATCCGTTTACA-GTAGTGCTGATATGATTGTTATGAATTACTT
SEQ:016-Sgd           (439)   GGTACTGATCCCAACCAAAGATCTTGTACACATCCGTTTACA-GTAGTGCTGATATGATTGTTATGAATTACTT
SEQ:017-Sgf           (439)   GGCACAGATCCAAATCAAAAATTCTTTACACATCCGTCTATA-GCTCAGCAGATCTTATTGTCGTCAACAGTCT
SEQ:018-Sgh           (439)   GGCACAGATCCAAATCAAAAATTCTTTACACATCCGTCTATA-GCTCAGCCGATTGATTGTCGTCAACAGTCT
SEQ:019-Mt2b1         (448)   GGAACAGATCCAAATCAAAAATTCTTTACACATCCGTCTACAGCTCAGCCGATTGATTGTCGTCAACAGTCT
SEQ:020-H2a           (439)   GGCACAGATCCAAATCAAAAATTCTTTACACATCCGTCTATA-GCTCAGCCGATCTCATTGTCGTCAACAGTCT
```

Figure 39

```
                                     526                                                                        600
SEQ:001-405(pumilus)   (513)  ATCAAAAATTAGACGGT-GCTCAAAAAC-GCTCAAATTCATGGCGTTGGGCACACATTGGTTTATTGATGAACAGCCAA
SEQ:002-406(subtilis)  (513)  ATCAAGATTAGATGGT-GCTAGAAAC-GTTCAAATCCATGGCGTTGGACACATCGGCCTTCGTACAGCAGCCAA
SEQ:003-402(megat.)    (513)  ATCAAAAATTAGACGGT-GCTAGAAAC-GTTCAAATTCATGGCGTTGGGCACATCGGCCTTCGTTATTGATGAACAGCCAA
SEQ:004-400(lentus)    (513)  ATCAAAAATTAGACGGT-GCTAAAAAC-GTTCAAATTCATGGCGTTGGGCACATCGGCCTTCGTTATTGATGAACAGCCAA
SEQ:005-396(circul.)   (513)  ATCAAAAATTAGACGGT-GCTAAAAAC-GTTCAAATTCATGGCGTTGGGCACATCGGCCTTCGTTATTGATGAACAGCCAA
SEQ:006-392(azotof.)   (513)  ATCAAAAATTAGACGGT-GCTAAAAAC-GTACAAATTCATGGCGTTGGGCACATTGGTTTATTGATGAACAGCCAA
SEQ:007-398(firmus)    (513)  ATCAAAAATTAGACGGT-GCTCAAAAAC-GCTCAAATTCATGGCGTTGGGCACATTGGTTTATTGATGAACAGCCAA
SEQ:008-393(badius)    (513)  ATCAAAAATTAGACGGT-GCTCAAAAAC-GTTCAAATTCATGGCGTTGGGCACATTGGTTTATTGATGAACAGCCAA
SEQ:009-Dc5h           (513)  ATCAAGATTAGATGGT-GCGAGAAAC-GTTCAAATCCATGGCGTTGGACACATCGGCCTTCGTATCGGTACAGCAGCCAA
SEQ:010-Dc5f           (513)  CTCTCGTTAATTGGC-GCAAGAAAC-ATCCTGATCCATGGCGTTGGTCATATCGGTCTATTAACCTCAAGCCAA
SEQ:011-Dc5c1          (522)  TTCGC-GTTAATTGGCGCAAGAAAC-GTCCTGATCCATGGCGTTGGTCATATCGGTCTATTAACCTCAAGCCAA
SEQ:012-Dc5a2          (522)  CTCGC-GTTAATTGGCGCAAGAAAC-GTCCTCATTCACGGCGTTGGTCACATCGGTCTATTAGCTTCAAGCCAA
SEQ:013-Dc512          (522)  CTCTCAGTTAATTGGCGCAAGAAAC-ATCCTGATCCA-GGCGTTGGTCGACATATCGGTCTATTAACCTCAAGCCAA
SEQ:014-Sga            (513)  AACAAAAATTAGACGGG-GCTAAAAAT-GTTCAAATTCATGGCGTTGGTCGGACATATCGGTCTATTAACCTCAAGCCAA
SEQ:015-Sgc            (513)  ATCAAAAATTAGACGGG-GCTAAAAAT-GTTCAAATTCATGGCGTTGGTCGGACATATCGGTCTATTAACCTCAAGCCAA
SEQ:016-Sgd            (513)  ATCAAAAATTAGACGGG-GCTAAAAAT-GTTCAAATTCATGGCGTTGGTCGGACATATCGGTCTATTAACCTCAAGCCAA
SEQ:017-Sgf            (513)  CTCTCGTTAATTGGC-GCAAGAAAC-GTCCAAATCCATGGCGTTGGACATATCGGTCTATTAACCTCAAGCCAA
SEQ:018-Sgh            (513)  CTCTCGTTAATTGGC-GCAAGAAAC-GTCCAAATCCATGGCGTTGGACATATCGGCCATATCGGTCTATTAACCTCAAGCCTA
SEQ:019-Mt2b1          (522)  TTCGC-GTTAACTGGCTGCAAGAAAT-GTCCTGACCCAAATCCATGGCGTTGGCCATATCGGTCTATTAACCTCAAGCCAA
SEQ:020-H2a            (514)  CTCTCGTTAATTGGCTGCAAGAAACAGTCCAAATCCAAATCCATGGCGTTGGACATATCGGTCTATTAACCTCAAGCCAA
```

Figure 3h

```
                                  601                                                654
SEQ:001-405 (pumilus)    (586)  GTCAACAGCCTGATTAAAGAAGAAGGACTGAACGGCGGGGGGCCCAAAATACGAATTAA
SEQ:002-406 (subtilis)   (586)  GTCAACAGCCTGATTAAAGAAGAAGGGCTGAACGGCGGGGGACTCAATACAAATTAG
SEQ:003-402 (megat.)     (586)  GTCAACAGCCTGATTAAAGAAGAAGGACTGAACGGCGGGGGGACCCACAATACAAATTAA
SEQ:004-400 (lentus)     (586)  GTCAACAGCCTGATTAAAGAAGAAGGACTGAACGGCGGCGGACTAAATACAAATTAA
SEQ:005-396 (circul.)    (586)  GTCAACAGCCTGATTAAAGAAGAAGGACTGAACGGCGGCGGCCTCAATACAAATTAA
SEQ:006-392 (azotof.)    (586)  GTCAACAGCCTGATTAAAGAAGAAGGACTGAACGGCGGGGGCCTCAATACAAATTAA
SEQ:007-398 (firmus)     (586)  GTCAACAGCCTGATTAAAGAAGAAGGACTGAACGGCGGCGGCCTAGATACAAATTAA
SEQ:008-393 (badius)     (586)  GTCAACAGCCTGATTAAAGAAGAAGGACTGAACGGCGGGGGCCACAATACAAATTAA
SEQ:009-Dc5h             (586)  GTCAACAGCCTGATTAAAGAAGAAGGGCTGAACGGCGGCGGCCACAATACAAATTAA
SEQ:010-Dc5f             (586)  GTGAAAGGGTATATTAAAGAAGAAGGGCTGAACGGCGGCGGCCTCAATACAAATTAA
SEQ:011-Dc5c1            (595)  GTCAAAGGCTATGTGAAAGAAGAAGGGCTGAACGGCGGGGGACAGAATACAAATTAA
SEQ:012-Dc5a2            (595)  GTCAAAGGCTATATCAAAGAAGAAGGACTGAACGGCGGCGGCCAAAATACAAATTAA
SEQ:013-Dc512            (595)  GTGAAAGGGTATATTAAAGAAGAAGGGCTTAACGGCGGCGGCCTCAATACAAATTAA
SEQ:014-Sga              (586)  GTCAACAGCCTGATTAAAGAAGAAGGGCTTAACGGCGGGGGACTCAATACAAATTAA
SEQ:015-Sgc              (586)  GTCAATAGCCTGATTAAAGAAGAAGGGCTTAACGGCGGCGGACTCAATACGAATTAA
SEQ:016-Sgd              (586)  GTCAACAGCCTGATTAAAGAAGAAGGGCTTAACGGCGGGGGCCTGAATACGAATTAA
SEQ:017-Sgf              (586)  GTCAAAGGATATATTAAAGAAGAAGGACTGAACGGCGGCGGCCTCAATACAAATTAA
SEQ:018-Sgh              (586)  GTCAAAGGATATATTAAAGAAGAAGGACTGAACGGCGGCGGCCCAAAATACAAATTAA
SEQ:019-Mt2b1            (595)  GTGAAAGGGTATATTAAAGAAGAAGGACTGAACGGCGGGGGCCTAAATACAAATTAA
SEQ:020-H2a              (589)  GTCAAAGGATATATTAAAGAAGAAGGACTGAACGGCGGGGGGACTAAATACAAATTAA
```

Figure 3i

```
                                1                                                                            75
SEQ:021-1f15(G2)  (1)  TGAACACAATCCAGTTGTTATGTTATGGTTCACGGTATTGGAGGGGCATCATTCAATTTGCGGGAATTAAGAGCTATCT
    SEQ:022-3C12  (1)  TGAACACAATCCAGTTGTTATGTTATGGTTCACGGTATTGGAGGGGCATCATTCAATTTGCGGGAATTAAGAGCTATCT
SEQ:023-3N19(G2)  (1)  TGAACACAATCCAGTTGTTATGTTATGGTTCACGGTATTGGAGGGGCATCATTCAATTTGCGGGAATTAAGAGCTATCT
  SEQ:024-G2.2    (1)  TGAACACAATCCAGTTGTTATGTTATGGTTCACGGTATCGGAGGGGCATCATTCAATTTGCGGGAATTAAGAGCTATCT
    SEQ:025-2C3   (1)  TGAACACAATCCAGTTGTTATGTTATGGTTCACGGTATCGGAGGGGCATCATTCAATTTGCGGGAATTAAGAGCTATCT
   SEQ:026-2F11   (1)  TGAACACAATCCAGTTGTTATGTTATGGTTCACGGTATTGGAGGAGCTTCATACAATTTGCGGGAATTAAGAGCTATCT
SEQ:027-KV11(6C7) (1)  TGAACACAATCCAGTTGTTATGTTATGGTTCACGGTATTGGAGGGGCATCATTCAGTTTGCGGGAATTAAGAGCTATCT
 SEQ:028-KV6(3A1) (1)  TGAACACAATCCAGTTGTTATGTTATGGTTCACGGTATTGGAGGGGCATCATTCAGTTTGCGGGAATTAAGAGCTATCT
 SEQ:029-KV2(2D1) (1)  TGAACACAATCCAGTTGTTATGTTATGGTTCACGGTATTGGAGGAGCTTCATACAGTTTGCGGGAATTAAGAGCTATCT
   SEQ:030-N2.5   (1)  TGAACACAATCCAGTTGTTATGTTATGGTTCACGGTATCGGAGGAGCTTCATACAGTTTGCGGGAATTAAGAGCTATCT
 SEQ:031-KV5(2H6) (1)  TGAACACAATCCAGTTGTTATGTTATGGTTCACGGTATTGGAGGAGCATCATTCAATTTGCGGGAATTAAGAGCTATCT
    SEQ:032-3E5   (1)  TGAACACAATCCAGTTGTTATGTTATGGTTCACGGTATTGGAGGGGCATCATTCAATTTGCGGGAATTAGGAGCTATCT
    SEQ:033-G2.1  (1)  TGAACACAATCCAGTTGTTATGTTATGGTTCACGGTATTGGAGGGGCATCATTCAATTTGCGGGAATTAGGAGCTATCT
SEQ:034-3H24(G2)  (1)  TGAACACAATCCAGTTGTTATGTTATGGTTCACGGTATTGGAGGGGCATCATTCAATTTGCGGGAATTAAGAGCTATCT
SEQ:035-KV10(4G6) (1)  TGAACACAATCCAGTTGTTATGTTATGGTTCACGGTATTGGAGGGGCATCATTCAATTTGCGGGAATTAAGAGCTATCT
SEQ:036-KV12(6D4) (1)  TGAACACAATCCAGTTGTTATGTTATGGTTCACGGTATTGGAGGGGCATCATTCAGTTTGCGGGAATTAAGAGCTATCT
   SEQ:037-N2.2   (1)  TGAACACAATCCAGTTGTTATGTTATGGTTCACGGTATCGGGGGGGCATCATTCAGTTTGCGGGAATTAGGAGCTATCT
   SEQ:038-N2.3   (1)  TGAACACAATCCAGTTGTTATGTTATGGTTCACGGTATCGGGGGGGCATCATTCAGTTTGCGGGAATTAGGAGCTATCT
   SEQ:039-N2.1   (1)  TGAACACAATCCAGTTGTTATGTTATGGTTCACGGTATCGGAGGGGCATCATTCAGTTTGCGGGAATTAGGAGCTATCT
SEQ:040-KV4(2E12) (1)  TGAACACAATCCAGTTGTTATGTTATGGTTCACGGTATTGGAGGGGACATCATTCAATTTGCGGGAATAAAGAGCTATCT
 SEQ:041-KV9(4C6) (1)  TGAACACAATCCAGTTGTTATGTTATGGTTCACGGTATTGGAGGGGCATCATTCAGTTTGCGGGAATTAAAGAGCTATCT
   SEQ:042-7D6    (1)  TAAACACAATCCAGTTGTTATGTTATGGTTCACGGTATCGGAGGGGCATCATCATACAATTTGCGGAATAAAAGAGCTATCT
   SEQ:043-3F3    (1)  TGAACACAATCCAGTTGTTATGTTATGGTTCACGGTATTGGAGGGGCATCATTCAATTTGCGGGAATTAAGAGCTATCT
SEQ:044-2D11(G2)  (1)  TGAACACAATCCAGTTGTTATGTTATGGTTCACGGTATCGGAGGGGCATCATTCAATTTGCGGGAATTAAGAGCTATCT
SEQ:045-3C23(G2)  (1)  TGAACACAATCCAGTTGTTATGTTATGGTTCACGGTATCGGAGGGGCATCATTCAATTTGCGGGAATTAAGAGCTATCT
   SEQ:046-G2.3   (1)  TGAACACAATCCAGTTGTCGTTATGTTATGGTTCACGGTATTGGAGGGGCATCATTCAATTTGCGGGAATTAAGAGCTATCT
   SEQ:047-2A3    (1)  TGAACACAATCCAGTTGTTATGTTATGGTTCACGGTATTGGAGGGGCATCGTTCAATTTGCGGGAATTAAGAGCTATCT
   SEQ:048-2F4    (1)  TGAACACAATCCAGTTGTTATGTTATGGTTCACGGTATTGGAGGGGCATCATTCAATTTGCGGGAATTAAGAGCTATCT
 SEQ:049-2B9(G2)  (1)  TGAACACAATCCAGTTGTTATGTTATGGTTCACGGTATTGGAGGGGCATCATTCAATTTGCGGGAATTAAGAGCTATCT
   SEQ:050-2C5    (1)  TGAACACAATCCAGTTGTTATGTTATGGTTCACGGTATTGGAGGGGCATCATTCAATTTGCGGGAATTAAGAGCTATCT
 SEQ:051-KV1(2A6) (1)  TGAACACAATCCAGTTGTTATGTTATGGTTCACGGTATTGGAGGGGCATCATTCAATTTGCGGGAATTAAGAGCTATCT
SEQ:052-2D13(G2)  (1)  TGAACACAATCCAGTTGTTATGTTATGGTTCACGGTATTGGAGGGGCATCATTCAATTTGCGGGAATTAAGAGCTATCT
   SEQ:053-3C8    (1)  TAAACACAATCCAGTTGTTATGTTATGGTTCACGGTATCGGAGGGGCATCATTCAATTTGCGGGAATTAAGAGCTATCT
   SEQ:054-2D5    (1)  TGAACACAATCCAGTTGTTATGTTATGGTTCACGGTATCGGAGGGGCATCATTCAATTTGCGGGAATTAAGAGCTATCT
```

Figure 4a

```
                                    76                                                                                             150
SEQ:021-1f15(G2)   (76)  CGTATCTCAGGGCTGGTCGCGGGGCAAGCTGTATGCGGTTGATTTTTGGGACAAGACAGGGACGAATTATAACAA
  SEQ:022-3C12     (76)  CGTATCTCAGGGCTGGTCACGGGGCAAGCTGTATGCGGTTGATTTTTGGGACAAGACAGGGACGAATTATAACAA
SEQ:023-3N19(G2)   (76)  CGTATCTCAGGGCTGGTCACGGGGCAAGCTGTATGCGGTTGATTTTTGGGACAAGACAGGGACGAATTATAACAA
  SEQ:024-G2.2     (76)  CGTATCTCAGGGCTGGTCACGGGGCAAGCTGTATGCGGTTGATTTTTGGGACAAGACAGGGACGAATTATAACAA
  SEQ:025-2C3      (76)  CGTATCTCAGGGCTGGTCGCGGGGCAAGCTGTATGCGGTTGATTTTTGGGACAAGACAGGGACGAATTATAACAA
  SEQ:026-2F11     (76)  CGTATCTCAGGGCTGGTCGCGGGGCAAGCTGTATGCGGTTGATTTTTGGGACAAGACAGGGACGAATTATAACAA
SEQ:027-KV11(6C7)  (76)  CGTATCTCAGGGCTGGTCACGGGGCAAGCTGTATCCGGTTGATTTTTGGGACAAGACAGGGACGAATTATAACAA
SEQ:028-KV6(3A1)   (76)  CGTATCTCAGGGCTGGTCACGGGGCAAGCTGTATGCGGTTGATTTTTGGGACAAGACAGGGACGAATTATAACAA
SEQ:029-KV2(2D1)   (76)  CGTATCTCAGGGCTGGTCACGGGGCAAGCTGTATGCGGTTGATTTTTGGGACAAGACAGGGACGAATTATAACAA
  SEQ:030-N2.5     (76)  CGTATCTCAGGGCTGGTCACGGGGCAAGCTGTATGCGGTTGATTTTTGGGACAAGACAGGGACGAATTATAACAA
SEQ:031-KV5(2H6)   (76)  CGTATCTCAGGGCTGGTCACGGGGCAAGCTGTATGCGGTTGATTTTTGGGACAAGACAGGGACGAAATTATAACAA
  SEQ:032-3E5      (76)  CGTATCTCAGGGCTGGTCACGGGGCAAGCTGTATACGGTTGATTTTTGGGACAAGACAGCACAGGGACGAATTATAACAA
  SEQ:033-G2.1     (76)  CGTATCTCAGGGCTGGTCACGGGGCAAGCTGTATGCGGTTGATTTTTGGGACAAGACAGGGACGAATTATAACAA
SEQ:034-3H24(G2)   (76)  CGTATCTCAGGGCTGGTCGCCGCGGGACAAGCCGTATGCGGTTGATTTTTGGGACAAGACAGGGACGAATTATAACAA
SEQ:035-KV10(4G6)  (76)  CGTGTCTCAGGGCTGGTCGCCGCGGGACAAGCTGTATGCGGTTGATTTTTGGGACAAGACAGGGACGAATTATAACAA
SEQ:036-KV12(6D4)  (76)  CGTATCTCAGGGCTGGTCGCCGCGGGACAAGCTGTATGCGGTTGATTTTTGGGACAAGACAGCACAAATTATAACAA
  SEQ:037-N2.2     (76)  CGAATCTCAGGGCTGGTCGCCGCGGGACAAGCTGTATGCGGTTGATTTTTGGGACAAGACAGCACAAATTATAACAA
  SEQ:038-N2.3     (76)  CGTATCTCAGGGCTGGTCGCCGCGGGACAAGCTGTATGCGGTTGATTTTTGGGACAAGACAGCACAAATTATAACAA
  SEQ:039-N2.1     (76)  CGTATCCCAGGGCTGGTCGCCGCGGGACAAGCTGTATGCGGTTGATTTTTGGGACAAGACAGCACAAATTATAACAA
SEQ:040-KV4(2E12)  (76)  CGTATCTCAGGGCTGGTCGCCGCGGGACAAGCCGTATGCGGTTGATTTTTGGGACAAGACAGCACAGGGACGAATTATAACAA
SEQ:041-KV9(4C6)   (76)  CGTATCTCAGGGCTGGTCTGCCGCGGGACAAGCTGTATGCGGTTGAGTTGATTTTTTAGTGACAAAACAGGGACGAATTATAACAA
  SEQ:042-7D6      (76)  CGTATCTCAGGGCTGGTCTGCCGCGGGACAAGCTGTATGCGGTTGAGTTGATTTTTTAGTGACAAGACAGGGACGAATTATAACAA
  SEQ:043-3F3      (76)  CGAATCTCAGGGCTGGTCTGCCGCGGGACAAGCTGTATGCGGTTGAGTTGATTTTTGGGACAAGACACCGGACGAATTATAACAA
SEQ:044-2D11(G2)   (76)  CGTATCTCAGGGCTGGTCGCCGCGGGACAAGCTGTATGCGGTTGATTTTTGGGACAAGACAGGGACGAATTATAACAA
SEQ:045-3C23(G2)   (76)  CGTATCTCAGGGCTGGTCGCCGCGGGACAAGCTGTATGCGGTTGATTTTTGGGACAAGACAGGGACGAATTATAACAA
  SEQ:046-G2.3     (76)  CGTATCTCAGGGCTGGTCGCCGCGGGACAAGCTGTATGCGGTTGATTTTTGGGACAAGACAGGGACGAATTATAACAA
  SEQ:047-2A3      (76)  CGTATCTCAGGGCTGGTCGCGCGGGACAAGCTGTATGCGGTTGATTTGATTTCAAAGACAAGACAGGGACGAATTATAACAA
  SEQ:048-2F4      (76)  CGTATCTCAGGGCTGGTCGCCGCGGGACAAGCTGTATGCGGTTGATTTTTGGGACAAGACAGGGACGAATTATAACAA
SEQ:049-2B9(G2)    (76)  CGTATCTCAGGGCTGGTCGCCGCGGGACAAGCTGTATGCGGTTGATTTTTGGGACAAGACAGGGACGAATTATAACAA
  SEQ:050-2C5      (76)  CGTATCTCAGGGCTGGTCGCCGCGGGACAAGCTGTATGCGGTTGATTTTTGGGACAAGACAGGGACGAATTATAACAA
SEQ:051-KV1(2A6)   (76)  CGTATCTCAGGGCTGGTCGCCGCGGGACAAGCTGTATGCGGTTGATTTTTGGGACAATTCAAGGACAGCACAAATTATAACAA
SEQ:052-2D13(G2)   (76)  CGTATCTCAGGGCTGGTCGCCGCGGGAGAGCTGTATGCGGTTGATTTTTGGGACGAGACAAGACAGGGACGAATTATAACAA
  SEQ:053-3C8      (76)  CGTATCTCAGGGCTGGTCGCGCGGGACAAGCTGTATGCGGTTGATTTTTGGGACGAGACAAGACAGGGACGAATTATAACAA
  SEQ:054-2D5      (76)  CGTATCTCAGGGCTGGTCGCGCGGGACAAGCTGTATGCGGTTGATTTTTGGGACAAGACAGGGACGAATTATAACAA
```

Figure 4b

151   225

```
SEQ:021-1f15(G2)    (151)  TGGCCCGGTATTATCGCGTTTTGTGAAAAAGTATTAGAGATGAAACGGGTGCGAAAAAAGTGGATATTGTCGCTCA
SEQ:022-3C12        (151)  TGGCCCGGTATTATCTAGATTCGTCAGAGATGCTCTAGACAAAGCGGGTGCGAAAAAAGTGGATATTGTCGCTCA
SEQ:023-3N19(G2)    (151)  TGGCCCGGTATTATCACGATTTGTGAAAAAGTATTAGATGAAACGGGTGCGAAAAAAGTGGACATTGTCGCTCA
SEQ:024-G2.2        (151)  TGGCCCGGTATTATCACGATTTGTGCAAAAGTTTTAGACGAAACGGGTGCGAAAAAAGTGGATATTGTCGCTCA
SEQ:025-2C3         (151)  TGGCCCGGTATTATCACGATTTGTGCAAAAGTTTTAGACGAAACGGGTGCGAAAAAAGTGGATATTGTCGCTCA
SEQ:026-2F11        (151)  TGGCCCGGTATTATCACGATTTGTGCAAAAGTTTTAGACGAAACGGGTGCGAAAAAAGTGGATATTGTCGCTCA
SEQ:027-KV11(6C7)   (151)  TGGCCCGGTATTATCACGATTTGTGCAAAAGTTTGGACGAAACGGGTGCGAAAAAAGTGGATATTGTCGCTCA
SEQ:028-KV6(3A1)    (151)  TGGCCCGGTATTATCACGATTTGTGCAAAAGTTTGGACGAAACGGGTGCGAAAAAAGTGGATATTGTCGCTCA
SEQ:029-KV2(2D1)    (151)  TGGCCCGGTATTATCACGATTTGTGCAAAAGTTTGGACGAAACGGGTGCGAAAAAAGTGGATATTGTCGCTCA
SEQ:030-N2.5        (151)  TGGCCCGGTATTATCACGATTTGTGCAAAAGTTTTAGACGAAACGGGTGCGAAAAAAGTGGATATTGTCGCTCA
SEQ:031-KV5(2H6)    (151)  TGGCCCGGTATTATCACGATTTGTGCAAAAGTTTTAGACGAAACGGGTGCGAAAAAAGTGGATATTGTCGCTCA
SEQ:032-3E5         (151)  TGGCCCGGTATTATCACGATTTGTGCAAAAGTTTTAGACGAAACGGGTGCGAAAAAAGTGGATATTGTCGCTCA
SEQ:033-G2.1        (151)  TGGCCCGGTATTATCACGATTTGTGCAAAAGTTTTAGACGAAACGGGTGCGAAAAAAGTGGATATTGTCGCTCA
SEQ:034-3H24(G2)    (151)  TGGCCCGGTATTATCACGATTTGTGCAAAAGTTTTAGACGAAACGGGTGCGAAAAAAGTGGATATTGTCGCTCA
SEQ:035-KV10(4G6)   (151)  TGGCCCGGTATTATCACGATTTGTGCAAAAGTTTTAGACGAAACGGGTGCGAAAAAAGTGGATATTGTCGCTCA
SEQ:036-KV12(6D4)   (151)  TGGCCCGGTATTATCACGATTTGTGCAAAAGTTTTAGACGAATGAAACGGGTGCGAAAAAAGTGGATATTGTCGCCCA
SEQ:037-N2.2        (151)  TGGCCCGGTATTATCACGATTTGTGCAAAAGTATTAGACGAATGAAACGGGTGCGAAAAAAGTGGATATTGTCGCCTA
SEQ:038-N2.3        (151)  TGGCCCGGTATTATCACGATTTGTGCAAAAGTTTTAGACGAATGAAACGGGTGCGAAAAAAGTGGATATTGTCGCCCA
SEQ:039-N2.1        (151)  TGGCCCGGTATTATCACGATTTGTGCAAAAGTTTTAGACGAATGAAACGGGTGCGAAAAAAGTGGATATTGTCGCCCA
SEQ:040-KV4(2E12)   (151)  TGGCCCGGTATTATCACGATTTGTGCAAAAGTTTTAGACGAAACGGGTGCGAAAAAAGTGGATATTGTCGCTCA
SEQ:041-KV9(4C6)    (151)  TGGCCCGGTATTATCACGATTTGTGCAAAAGTTTTAGACGAAACGGGTGCGAAAAAAGTGGATATTGTCGCTCA
SEQ:042-7D6         (151)  TGGCCCGGTATTATCACGATTTGTGCAAAAGTTTTAGACGAAACGGGTGCGAAAAAAGTGGATATTGTCGCTCA
SEQ:043-3F3         (151)  TGGCCCGGTATTATCACGATTTGTGCAAAAGTATTAGACGAATGAAACGGGTGCGAAAAAAGTGGATATTGTCGCTCA
SEQ:044-2D11(G2)    (151)  TGGCCCGGTATTATCACGATTTGTGCAAAAGTTTTAGAAGGCTTTAGACGAATGAAACGGGTGCGAAAAAAGTGGATATTGTCGCTCA
SEQ:045-3C23(G2)    (151)  TGGCCCGGTATTATCACGATTTGTGCAAAAGTTTTAGACGAATGAAACGGGTGCGAAAAAAGTGGATATTGTCGCTCA
SEQ:046-G2.3        (151)  TGGCCCGGTATTATCACGATTTGTGCAAAAGTTTTAGAAGGTTTAGACGAAACGGGTGCGAAAAAAGTGGATATTGTCGCTCA
SEQ:047-2A3         (151)  TGGCCCGGTATTATCACGATTTGTGCAAAAGTATTAGAAGGTTTAGACGAATGAATGAAACGGGTGCGAAAAAAGTGGATATTGTCGCTCA
SEQ:048-2F4         (151)  TGGCCCGGTATTATCACGATTTGTGCAAAAGTTTTAGAAGGTATTAGACGAATGAATGAAACGGGTGCGAAAAAAGTGGATATTGTCGCTCA
SEQ:049-2B9(G2)     (151)  TGGCCCGGTATTATCACGATTTGTGCAAAAGTTTTAGAAGGTATTAGACGAATGAATGAAACGGGTGCGAAAAAAGTGGATATTGTCGCTCA
SEQ:050-2C5         (151)  TGGCCCGGTATTATCGCGTTTTGTGCAAAAGTATTAGAAGGTATTAGACGAATGAATGAAACGGGTGCGAAAAAAGTGGATATTGTCGCTCA
SEQ:051-KV1(2A6)    (151)  TGGCCCGGTATTATCACGATTTGTGCAAAAGTATTAGAAGGTATTAGACGAATGAATGAAACGGGTGCGAAAAAAGTGGATATTGTCGCTCA
SEQ:052-2D13(G2)    (151)  TGGCCCGGTATTATCACGATTTGTGCAAAAGTTTTAGAAGGTTTAGACGAAACGGGTGCGAAAAAAGTGGATATTGTCGCTCA
SEQ:053-3C8         (151)  TGGCCCGGTATTATCACGATTTGTGCAAAAGTTTTAGAAGGTTTAGACGAAACGGGTGCGAAAAAAGTGGATATTGTCGCTCA
SEQ:054-2D5         (151)  TGGCCCGGTATTATCACGATTTGTGCAAAAGTTTTAGACGAAACGGGTGCGAAAAAAGTGGATATTGTCGCTCA
```

Figure 4c

```
                                   226                                                                        300
SEQ:021-1f15(G2)   (226)  CAGCATGGGCGGCGCTAACACGCTTTACTACATAAAAAATCTGGACGGCGGCGGAAATAAAGTTGAAAACGTCGTAAC
SEQ:022-3C12       (226)  CAGCATGGGGGGCGCGAACACACACTTTACTACATAAAAAATCTGGACGGCGGCGGAAATAAAATTGAAAACGTCGTAAC
SEQ:023-3N19(G2)   (226)  CAGCATGGGTGCGCGCGAACACACTTTACTACATAAAAAATCTGGACGGCGGCGGAAATAAAATTGAAAACGTCGTAAC
SEQ:024-G2.2       (226)  CAGCATGGGGGGCGGCGAACACACTTTACTACATAAAAAATCTGGACGGCGGCGGAAATAAAATTGAAAACGTCGTAAC
SEQ:025-2C3        (226)  CAGCATGGGCGGCGGCGAACACACTTTACTACATAAAAAATCTGGACGGCGGCGGAAATAAAATTGAAAACGTCGTCAC
SEQ:026-2F11       (226)  CAGCATGGGCGGCGGCGAACACACTTTACTACATAAAAAATTTGGATGGCGGCGGAAATTGAAAACGTCGTAAC
SEQ:027-KV11(6C7)  (226)  CAGTATGGGCGGCGGCGAACACACTTTACTACATAAAAAATCTGGACGGCGGCGGAAATAAAATTGAAAACGTCGTAAC
SEQ:028-KV6(3A1)   (226)  CAGTATGGGTGCGCGCGAACACACTTTACTACATAAAAAATCTGGACGGCGGCGGAAATAAAATTGAAAACGTCGTAAC
SEQ:029-KV2(2D1)   (226)  CAGCATGGGTGCGCGCGAACACACTTTACTACATAAAAAATCTGGACGGCGGCGGAAATAAAATTGAAAACGTCGTAAC
SEQ:030-N2.5       (226)  CAGCATGGGTGCGCGCGAACACACTTTACTACATAAAAAATCTGGACGGCGGCGGAAATAAAATTGAAAACGTCGTAAC
SEQ:031-KV5(2H6)   (226)  CAGCATGGGTGCGCGCGAACACACTTTACTACATAAAAAATCTGGACGGCGGCGGAAATAAAATTGAAAACGTCGTAAC
SEQ:032-3E5        (226)  CAGCATGGGCGGCGGCGAACACACTTTACTACATAAAAAATCTGGACGGCGGCGGAAATAAAATTGAAAACGTCGTAAC
SEQ:033-G2.1       (226)  CAGCATGGGGGGCGGCGAACACACTTTACTACATAAAAAATCTGGACGGCGGCGGAAATAAAGTTGAAAACGTCGTAAC
SEQ:034-3H24(G2)   (226)  CAGCATGGGGGGCGGCGCGAACACACTTTACTACATAAAAAATCTGGACGGCGGCGGAAATAAAGTTGAAAGCGTCGTAAC
SEQ:035-KV10(4G6)  (226)  CAGCATGGGTGCGCGCGAACACACTTTACTACATAAAAAATCTGGACGGCGGCGGAAATAAAGTTGAAAGCGTCGTAAC
SEQ:036-KV12(6D4)  (226)  CAGCATGGGTGCGCGCGAACACACTTTACTACATAAAAAATCTGGACGGCGGCGGAAATAAAGTTGAAAGCGTCGTGAC
SEQ:037-N2.2       (226)  CAGCATGGGTGCGCGCGAACACACTTTACTACATAAAAAATCTGGACGGCGGCGGAAATAAAGTTGAAAACGTCGTGAC
SEQ:038-N2.3       (226)  CAGCATGGGTGCGCGCGAACACACTTTACTACATAAAAAATCTGGACGGCGGCGGAAATAAAGTTGGAAACGTCGTGAC
SEQ:039-N2.1       (226)  CAGCATGGGCGGCGGCGAACACACTTTACTACATAAAAAATCTGGACGGCGGCGGAAATAAAGTTGGAAACGTCGTGAC
SEQ:040-KV4(2E12)  (226)  CAGCATGGGCGGCGGCCAACACGCTTTACTACATAAAAAATCTGGACGGCGGCGGAAATAAAATTGAAAACGTCGTGAC
SEQ:041-KV9(4C6)   (226)  CAGCATGGGCGGCGGCGAACACACTTTACTACATAAAAAATCTGGATGGCGGCGGTAATAAAATTGAAAACGTCGTAAC
SEQ:042-7D6        (226)  CAGCATGGGGGGCGGCGAACACACTTTACTACATAAAAAATCTGGACGGCGGCGGTAATAAAATTGAAAACGTCGTAAC
SEQ:043-3F3        (226)  CAGCATGGGTGCGCGCGAACACACTTTACTACATAAAAAATCTGGACGGCGGCGGAAATAAAATTGAAAACGTCGTAAC
SEQ:044-2D11(G2)   (226)  CAGCATGGGGGGCGGCGAACACACTTTACTACATAAAAAATCTGGACGGCGGCGGAAATAAAATTGAAAACGTCGTCAC
SEQ:045-3C23(G2)   (226)  CAGCATGGGGGGCGGCGAACACACTTTACTACATAAAAAATCTGGACGGCGGCGGAAATAAAATTGAAAACGTCGTCAC
SEQ:046-G2.3       (226)  CAGCATGGGTGCGCGCGAACACACTTTACTACATAAAGAATCTGGACGGCGGCGGAAATAAAATTGAAAACGTCGTAAC
SEQ:047-2A3        (226)  CAGCATGGGCGGCGCGCTAACACGCTTTACTACATAAAAGAATCTGGACGGCGGCGGAAATAAAATTGAGAACGTCGTAAC
SEQ:048-2F4        (226)  CAGCATGGGCGGCGCGCTAACACGCTTTACTACATAAAAAATCTGGACGGCGGCGGAAATAAAATTGAGAACGTCGTAAC
SEQ:049-2B9(G2)    (226)  CAGCATGGGGGGCGGCGAACACACTTTACTACATAAAAAATCTGGACGGCGGCGGCGATAAATAAAATTGAAAACGTCGTAAC
SEQ:050-2C5        (226)  CAGCATGGGTGCGCGCGAACACACTTTACTACATAAAAAATCTGGACGGCGGCGGTAATAAAATTGAAAACGTCGTAAC
SEQ:051-KV1(2A6)   (226)  CAGCATGGGTGCGCGGCGAACACACTTTACTACATAAAAAATCTGGACGGCGGCGGAAATAAAATTGAAAACGTCGTCAC
SEQ:052-2D13(G2)   (226)  CAGCATGGGTGCGCGGCGAACACACTTTACTACATAAAAAATCTGGACGGCGGCGGAAATAAAATTGAAAACGTCGTAAC
SEQ:053-3C8        (226)  CAGCATGGGTGCGCGGCGAACACACTTTACTACATAAAAAATCTGGACGGCGGCGGAAATAAAGTTGAAAACGTCGTAAC
SEQ:054-2D5        (226)  CAGCATGGGTGCGCGCGAACACACTTTACTACATAAAAAATCTGGACGGCGGCGGAAATAAAACGTCGTAAC
```

Figure 4d

```
                                                                                    375
                301
SEQ:021-1f15(G2)  (301)  GCTTGGCGGCGCGCGCACGAACCGTTCGACGACGACAAGCAAGGCGCTTCCGGGAACACAGATCCAAATCAAAAGAGATTTTATACAC
SEQ:022-3C12      (301)  GCTTGGCGGCGCGCGCACGAACCGTTCGACGACGACAAGCAAGGCGCTTCCGGGAACACAGATCCAAATCAAAAGAGATTTTATACAC
SEQ:023-3N19(G2)  (301)  GCTTGGCGGCGCGCGCGAACCGTTTGACGACGACAAGCAAGGCGCTTCCGGGAACAGATCCAAATCAAAAGAGATTTTATACAC
SEQ:024-G2.2      (301)  GCTTGGCGGCGCGCGCGAACCGTTCGACGACGACAAGCAAGGCGCTTCCGGGAACAGATCCAAATCAAAAGAGATTTTATACAC
SEQ:025-2C3       (301)  CATTGGTGGAGCGGCGCAAACGGACTCGTTCAAGCAGAGCAGGGCGCTTCAGGCACAGATCCAAATCAAAAAATTCTTTACAC
SEQ:026-2F11      (301)  GCTTGGCGGCGCGCGCGAACCGTTTGACGACGACAAGCAAGGCGCTTCCGGGAACAGATCCAAATCAAAAGAGATTTTATACAC
SEQ:027-KV11(6C7) (301)  GCTTGGCGGCGCGCGCGAACCGTTTGACGACGACAAGCAAGGCGCTTCCGGGTACTGATCCCAACCAAAAGATCTTGTACAC
SEQ:028-KV6(3A1)  (301)  GCTTGGCGGCGCGCGCGAACCGTTTGACGACGACAAGCAAGGCGCTTCCGGGTACTGATCCCAACCAAAAGATCTTGTACAC
SEQ:029-KV2(2D1)  (301)  GCTTGGCGGCGCGCGCGAACCGTTTGACGACGACAAGCAAGGCGCTTCCGGGAACAGATCCCAACCAAAAGATCTTGTACAC
SEQ:030-N2.5      (301)  GCTTGGCGGCGCGCGCGAACCGTTCGACGACGACAAGCAAGGCGCTTCCGGGAACTGATCCCAACCAAAAGATCTTGTACGC
SEQ:031-KV5(2H6)  (301)  GCTTGGCGGCGCGCGCGAATCGTCTTGTAACGACGACAAGCAAGGCGCTTCCGGGAACAGATCCAATCAAAAGATTTGTACGC
SEQ:032-3E5       (301)  GCTTGGCGGCGCGCGCACGAACCGTTTGACGACGACAAGCAAGGCGCTTCCGGGAACAGATCCAAATCAAAAGAGATTTTATACAC
SEQ:033-G2.1      (301)  GCTTGGCGGCGCGCGCGAACCGTTTGACGACGACAAGCAAGGCGCTTCCGGGAACAGATCCAAATCAAAAGAGATTTTATACAC
SEQ:034-3H24(G2)  (301)  ACTTGGCGGCGCGCGCGAATCGTCTTGTAACAGGCAAGGCGCTTCCGGGAACTGATCCCAACCAAAAGATTTTATACAC
SEQ:035-KV10(4G6) (301)  GCTTGGCGGCGCGCGCGAACCGTTTGACGACGACAAGCAAGGCGCTTCCGGGAACTGATCCCAACCAAAAGATTTTATACAC
SEQ:036-KV12(6D4) (301)  GCTTGGCGGCGCGCGCGAACCGTTTGACGACGACAAGCAAGGCGCTTCCGGGTACTGATCCCAACCAAAAGATTTTATACAC
SEQ:037-N2.2      (301)  GCTTGGCGGCGCGCGCGAACCGTTTGACGACGACAAGCAAGGCGCTTCCGGGTACTGATCCCAACCAAAAGATTTTATACAC
SEQ:038-N2.3      (301)  GCTTGGCGGCGCGCGCGAACCGTTTGACGACGACAAGCAAGGCGCTTCCGGGTACTGATCCCAACCAAAAGATTTTATACAC
SEQ:039-N2.1      (301)  GCTTGGCGGCGCGCGCGAACCGTTTGACGACGACAAGCAAGGCGCTTCCGGGTACTGATCCCAACCAAAAGATTTTATACAC
SEQ:040-KV4(2E12) (301)  GCTTGGCGGCGCGCGCGAACCGTTTGACGACGACAAGCAAGGCGCTTCCGGGAACAGATCCAAATCAAAAGAGATTTTATACAC
SEQ:041-KV9(4C6)  (301)  ACTTGGCGGCGCGCGCGAACCGTTTGACGACGACAAGCAAGGCGCTTCCGGGTACTGATCCCAACCAAAAGATCTTGTACAC
SEQ:042-7D6       (301)  ACTTGGCGGCGCGCGCGAACCGTTTGACGACGACAAGCAAGGCGCTTCCGGGTACTGATCCCAACCAAAAGATCTTGTACAC
SEQ:043-3F3       (301)  GCTTGGCGGCGCGCGCGAACCGTTTGACGACGACAAGCAAGGCGCTTCCGGGAACAGATCCAAATCAAAAGAGATTTTATACAC
SEQ:044-2D11(G2)  (301)  ACTTGGCGGCGCGCGCGAACCGTTCGACGACGACAAGCAAGGCGCTTCCGGGAACAGATCCAAATCAAAAGAGATTTTATACAC
SEQ:045-3C23(G2)  (301)  ACTTGGCGGCGCGCGCGAACCGTTCGACGACGACAAGCAAGGCGCTTCCGGGAACAGATCCAAATCAAAAGAGATTTTATACAC
SEQ:046-G2.3      (301)  GCTTGGCGGCGCGCGCGAACCGTTCGACGACGACAAGCAAGGCGCTTCCGGGAACAGATCCAAATCAAAAGAGATTTTATACAC
SEQ:047-2A3       (301)  GCTTGGCGGCGCGCGCGAACCGTTCGACGACGACAAGCAAGGCGCTTCCGGGTACTGATCCCAACCAAAAGATCTTGTACAC
SEQ:048-2F4       (301)  ACTTGGCGGCGCGCGCGAACCGTTTGACGACGACAAGCAAGGCGCTTCCGGGAACAGATCCCAACCAAAAGATCTTGTACAC
SEQ:049-2B9(G2)   (301)  ACTTGGCGGCGCGCGCGAACCGTTTGACGACGACAAGCAAGGCGCTTCCGGGAACAGATCCAAATCAAAAGAGATTTTATACAC
SEQ:050-2C5       (301)  ACTTGGCGGCGCGCGCGAACCGTTTGACGACGACAAGCAAGGCGCTTCCGGGAACTGATCCCAACCAAAAGATCTTGTACAC
SEQ:051-KV1(2A6)  (301)  GCTTGGCGGCGCGCGCGAATCGTCTTCGACGACGACAAGCAAGGCGCTTCCGGGTACTGATCCCAACCAAAAGATCTTGTACAC
SEQ:052-2D13(G2)  (301)  GCTTGGCGGCGCGCGCGAACCGTTCGACGACGACAAGCAAGGCGCTTCCGGGAACAGATCCAAATCAAAAGAGATTTTATACAC
SEQ:053-3C8       (301)  ACTTGGCGGCGCGCGCGAATCGTCTTCGACGACGACAAGCAAGGCGCTTCCGGGAACAGATCCAAATCAAAAGAGATTTTATACAC
SEQ:054-2D5       (301)  ACTTGGCGGCGCGCGCGAACCGTTCGACGACGACAAGCAAGGCGCTTCCGGGAACAGATCCAAATCAAAAGAGATTTTATACAC
```

Figure 4e

```
                                                              450
                   376
SEQ:021-1f15(G2)   (376)  ATCCATTTACAGCAGCAGTGCCGATATGATTGTCATGAATTACTTATCAAAATTAGACGGTGCTAAAAATGTTCAAAT
SEQ:022-3C12       (376)  ATCCATTTACAGCAGCAGTGCCGATATGATTGTCATGAATTACTTATCAAAATTAGACGGGGCTAAAAATGTTCAAAT
SEQ:023-3N19(G2)   (376)  ATCCATTTACGGCAGCAGTGCCGATATGATTGTCATGAATTACTTATCAAAATTAGACGGTGCTAAAAACGTTCAAAT
SEQ:024-G2.2       (376)  ATCCATTTACGGCAGCAGTGCCGATATGATTGTCATGAATTACTTATCAAAATTAGACGGTGCTAAAAACGTACAAAT
SEQ:025-2C3        (376)  ATCCGTCTATAGCTCAGCAGATCTTATTGTCGTCAACAGTCTCTCTCGTTTAATTAGACGGTGCAAGAAACGTACAAAT
SEQ:026-2F11       (376)  ATCCATTTACAGCAGCAGTGCCGATATGATTGTCATGAATTACTTATCAAAATTAGACGGTGCTAAAAATGTACAAAT
SEQ:027-KV11(6C7)  (376)  ATCCGTTTACAGTAGTGCTGATATGATTGTCATGAATTGTTATGAATTACTTATCAAAATTAGACGGGGCTAAAAATGTTCAAAT
SEQ:028-KV6(3A1)   (376)  ATCCGTTTACAGTAGTGCTGATATGATTGTCATGAATTGTTATGAATTGTTATGAATTACTTATCAAAATTAGACGGGGCTAAAAATGTTCAAAT
SEQ:029-KV2(2D1)   (376)  ATCCGTTTACAGTAGTGCTGCCGATATGATTGTCATGAATTGTTATGAATTACTTATCAAAATTAGACGGGGCTAAAAATGTTCAAAT
SEQ:030-N2.5       (376)  ATCCGTTTACAGTAGTGCTGATATGATTGTCATGAATTGTTATGAATTGTTATGAATTACTTATCAAAATTAGACGGGGCTAAAAATGTTCAAAT
SEQ:031-KV5(2H6)   (376)  ATCCGTTTACAGCAGCAGTGCCGATATGATTGTCATGAATTGTTATGAATTACTTATCAAAATTAGACGGTGCTAAAAATGTTCAAAT
SEQ:032-3E5        (376)  ATCCATTTACAGCAGCAGTGCCGATATGATTGTCATGAATTGTTATGAATTACTTATCAAAATTAGACTAGACGGTGCTAAAAATGTTCAAAT
SEQ:033-G2.1       (376)  ATCCATTTACAGCAGCAGTGCCGATATGATTGTCATGAATTGTTATGAATTACTTATCAAAATTAGACGGTGCTAAAAATGTTCAAAT
SEQ:034-3H24(G2)   (376)  ATCCATTTACAGCAGCAGTGCCGATATGATTGTCATGAATTGTTATGAATTGTTATGAATTACTTATCAAAATTAGACTAGACGGTGCTAAAAATGTTCAAAT
SEQ:035-KV10(4G6)  (376)  ATCCATTTACAGCAGCAGTGCCGATATGATTGTCATGAATTGTTATGAATTGTTATGAATTACTTATCAAAATTAGACGGTGCTAAAAATGTTCAAAT
SEQ:036-KV12(6D4)  (376)  ATCCGTTTACAGCAGCAGTGCCGATATGATTGTCATGAATTGTTATGAATTGTTATGAATTACTTATCAAAATTAGACGGTGCTAAAAATGTTCAAAT
SEQ:037-N2.2       (376)  ATCCGTTTACAGCAGCAGTGCCGATATGATTGTCATGAATTGTTATGAATTGTTATGAATTACTTATCAAAATTAGACGGTGCTAAAAATGTTCAAAT
SEQ:038-N2.3       (376)  ATCCGTTTACAGCAGCAGTGCCGATATGATTGTCATGAATTGTTATGAATTGTTATGAATTACTTATCAAAATTAGACGGTGCTAAAAATGTTCAAAT
SEQ:039-N2.1       (376)  ATCCGTTTACAGCAGCAGTGCCGATATGATTGTCATGAATTGTTATGAATTGTTATGAATTACTTATCAAAATTAGACGGTGCTAAAAATGTTCAAAT
SEQ:040-KV4(2E12)  (376)  ATCCATTTACAGCAGCAGTGCCGATATGATTGTTGTCATGAATTGTTATGAATTGTTATGAATTACTTATCAAAATTAGACTAGACGGGGCTAAAAATGTTCAAAT
SEQ:041-KV9(4C6)   (376)  ATCCATTTACAGCAGCAGTGCCGATATGATTGTCATGAATTGTTATGAATTGTTATGAATTACTTATCAAAAACTAGACTAGACGGTGCTAAAAATGTTCAAAT
SEQ:042-7D6        (376)  ATCCATTTACAGCAGCAGTGCCGATATGATTGTCATGAATTGTTATGAATTGTTATGAATTACTTATCAAAATTAGACGGTGCTAAAAACGTTCAAAT
SEQ:043-3F3        (376)  ATCCATTTACAGCAGCAGTGCCGATATGATTGTCATGAATTGTTATGAATTGTTATGAATTACTTATCAAAATTAGACGGTGCTAAAAACGTTCAAAT
SEQ:044-2D11(G2)   (376)  ATCCATTTACAGCAGCAGTGCCGATATGATTGTCATGAATTGTTATGAATTGTTATGAATTACTTATCAAAATTAGACGGTGCTAAAAACGTTCAAAT
SEQ:045-3C23(G2)   (376)  ATCCATTTACAGCAGCAGTGCCGATATGATTGTCATGAATTGTTATGAATTGTTATGAATTACTTATCAAAATTAGACGGTGCTAAAAACGTTCAAAT
SEQ:046-G2.3       (376)  ATCCATTTACAGCAGCAGTGCCGATATGATTGTCATGAATTGTTATGAATTGTTATGAATTACTTATCAAAATTAGACGGTGCTAAAAACGTTCAAAT
SEQ:047-2A3        (376)  ATCCATTTACAGTAGTGCTGATATGATTGTCATGAATTGTTATGAATTGTTATGAATTACTTATCAAAATTAGACGGTGCTAAAAATGTTCAAAT
SEQ:048-2F4        (376)  ATCCGTTTACAGTAGTGCTGATATGATTGTTATGAATTGTTATGAATTGTTATGAATTACTTATCAAAATTAGACGGTGCTAAAAATGTTCAAAT
SEQ:049-2B9(G2)    (376)  ATCCATTTACAGCAGCAGTGCCGATATGATTGTCATGAATTGTTATGAATTGTTATGAATTACTTATCAAAATTAGACGGTGCTAAAAATGTTCAAAT
SEQ:050-2C5        (376)  ATCCATTTACAGCAGCAGTGCCGATATGATTGTCATGAATTGTTATGAATTGTTATGAATTACTTATCAAAATTAGACGGTGCTAAAAATGTTCAAAT
SEQ:051-KV1(2A6)   (376)  ATCCATTTACAGCAGCAGTGCCGATATGATTGTCATGAATTGTTATGAATTGTTATGAATTACTTATCAAAATTAGACGGTGCTAAAAATGTTCAAAT
SEQ:052-2D13(G2)   (376)  ATCCATTTACAGCAGCAGTGCCGATATGATTGTCATGAATTGTTATGAATTGTTATGAATTACTTATCAAAATTAGACGGTGCTAAAAATGTTCAAAT
SEQ:053-3C8        (376)  ATCCATTTACAGCAGCAGTGCCGATATGATTGTCATGAATTGTTATGAATTGTTATGAATTACTTATCAAAAATTAGACGGTGCTAAAAATGTTCAAAT
SEQ:054-2D5        (376)  ATCCATTTACAGCAGCAGTGCCGATATGATTGTCATGAATTGTTATGAATTGTTATGAATTACTTATCAAAAATTAGACGGTGCTAAAAATGTTCAAAT
```

Figure 4f

```
                                451                                                                                            525
SEQ:021-1f15(G2)  (451)  TCATGGCGTTGGGCACATTGGTTTATTGATGAACAGCCAAGTCAACAGCCTGATTAAAGAAGGACTGAACGGCGG
SEQ:022-3C12      (451)  TCATGGCGTTGGGCACATTGGTTTATTGATGAACAGCCAAGTCAACAGCCTGATTAAAGAAGGACTGAACGGCGG
SEQ:023-3N19(G2)  (451)  CCATGGCGTTGGGCACATTGGTTTATTGATGAACAGCCAAGTCAACAGCCTGATTAAAGAAGGACTGAACGGCGG
SEQ:024-G2.2      (451)  TCATGGCGTTGGGACATATCGGTCTATTGGTTTATTGATGAACAGCCAAGTCAACAGCCTGATTAAAGAAGGACTGAACGGCGG
SEQ:025-2C3       (451)  CCATGGCGTTGGGCACATTGGTTTATTGATGAACCTCAAGCCAAGTCAACAGCCTGATTAAAGAAGGACTGAACGGCGG
SEQ:026-2F11      (451)  TCATGGCGTTGGGCACATTGGTTTATTGATGAACAGCCAAGTCAACAGCCTGATTAAAGAAGGACTGAACGGCGG
SEQ:027-KV11(6C7) (451)  TCATGGCGTTGGGCACATTGGTTTATTGATGAACAGCCAAGTCAACAGCCTGATTAAAGAAGGACTGAACGGCGG
SEQ:028-KV6(3A1)  (451)  TCATGGCGTTGGGCACATTGGTTTATTGATGAACAGCCAAGTCAACAGCCTGATTAAAGAAGGACTGAACGGCGG
SEQ:029-KV2(2D1)  (451)  TCATGGTGTCGGACATATCGGCCTTCTGTACAGCCAAGTCAACAGCCTGATTAAAGAAGGACTGAACGGCGG
SEQ:030-N2.5      (451)  TCATGGCGTTGGGCACTGGTTTATTGATGAACAGCCAAGTCAACAGCCTGATTAAAGAAGGACTGAACGGCGG
SEQ:031-KV5(2H6)  (451)  TCATGGCGTTGGGCACATTGGTTTATTGATGAACAGCCAAGTCAACAGCCTGATTAAAGAAGGACTGAACGGCGG
SEQ:032-3E5       (451)  CCATGGCGTTGGGACACATCGGCCTTCTGTACAGCCAAGTCAACAGCCTGATTAAAGAAGGACTGAACGGCGG
SEQ:033-G2.1      (451)  TCATGGCGTTGGGCACATTGGTTTATTGATGAACAGCCAAGTCAACAGCCTGATTAAAGAAGGACTGAACGGCGG
SEQ:034-3H24(G2)  (451)  TCATGGCGTTGGGCACATTGGTTTATTGATGAACAGCCAAGTCAACAGCCTGATTAAAGAAGGACTGAACGGCGG
SEQ:035-KV10(4G6) (451)  TCATGGCGTCGGACATATCGGCCTTCTGTACAGCCAAGTCAACAGCCTGATTAAAGAAGGACTGAACGGCGG
SEQ:036-KV12(6D4) (451)  TCATGGCGTTGGGCACATTGGTTTATTGATGAACAGCCAAGTCAACAGCCTGATTAAAGAAGGACTGAACGGCGG
SEQ:037-N2.2      (451)  TCATGGCGTTGGGCACATTGGTTTATTGATGAACAGCCAAGTCAACAGCCTGATTAAAGAAGGACTGAACGGCGG
SEQ:038-N2.3      (451)  TCATGGCGTTGGGCACATTGGTTTATTGATGAACAGCCAAGTCAACAGCCTGATTAAAGAAGGACTGAACGGCGG
SEQ:039-N2.1      (451)  TCATGGCGTTGGGCACATTGGTTTATTGATGAACAGCCAAGTCAACAGCCTGATTAAAGAAGGACTGAACGGCGG
SEQ:040-KV4(2E12) (451)  TCATGGCGTTGGGCACATTGGTTTATTGATGAACAGCCAAGTCAACAGCCTGATTAAAGAAGGACTGAACGGCGG
SEQ:041-KV9(4C6)  (451)  TCATGGTGTCGGGCACATTGGTTTATTGATGAACAGCCAAGTCAACAGCCTGATTAAAGAAGGACTGAACGGCGG
SEQ:042-7D6       (451)  TCATGGCGTTGGGCACATTGGTTTATTGATGAACAGCCAAGTCAACAGCCTGATTAAAGAAGGACTGAACGGCGG
SEQ:043-3F3       (451)  CCATGGCGTTGGGCACATTGGTTTATTGATGAACAGCCAAGTCAACAGCCTGATTAAAGAAGGGCTGAACGGCGG
SEQ:044-2D11(G2)  (451)  TCATGGCGTTGGGCACATTGGTTTATTGATGAACAGCCAAGTCAACAGCCTGATTAAAGAAGGACTGAACGGCGG
SEQ:045-3C23(G2)  (451)  TCATGGCGTTGGGCACATTGGTTTATTGATGAACAGCCAAGTCAACAGCCTGATTAAAGAAGGGCTTAACGGCGG
SEQ:046-G2.3      (451)  TCATGGCGTTGGGCACATTGGTTTATTGATGAACAGCCAAGTCAACAGCCTGATTAAAGAAGGACTGAACGGCGG
SEQ:047-2A3       (451)  TCATGGCGTTGGGCACATTGGTTTATTGATGAACAGCCAAGTCAACAGCCTGATTAAAGAAGGACTGAACGGCGG
SEQ:048-2F4       (451)  TCATGGCGTTGGGCACATTGGTTTATTGATGAACAGCCAAGTCAACAGCCTGATTAAAGAAGGACTGAACGGCGG
SEQ:049-2B9(G2)   (451)  TCATGGCGTTGGGCACATTGGTTTATTGATGAACAGCCAAGTCAACAGCCTGATTAAAGAAGGGCTTAACGGCGG
SEQ:050-2C5       (451)  TCATGGCGTTGGGCACATTGGTTTATTGATGAACAGCCAAGTCAACAGCCTGATTAAAGAAGGACTGAACGGCGG
SEQ:051-KV1(2A6)  (451)  TCATGGCGTTGGGCACATTGGTTTATTGATGAACAGCCAAGTCAACAGCCTGATTAAAGAAGGGCTTAACGGCGG
SEQ:052-2D13(G2)  (451)  TCATGGCGTTGGGCACATTGGTTTATTGATGAACAGCCAAGTCAACAGCCTGATTAAAGAAGGACTGAACGGCGG
SEQ:053-3C8       (451)  TCATGGCGTTGGGCACATTGGTTTATTGATGAACAGCCAAGTCAACAGCCTGATTAAAGAAGGACTGAACGGCGG
SEQ:054-2D5       (451)  TCATGGCGTTGGGCACATTGGTTTATTGATGAACAGCCAAGTCAACAGCCTGATTAAAGAAGGACTGAACGGCGG
```

Figure 49

```
                                    526              544
SEQ:021-1f15(G2)   (526)   GGGACTCAATACGAATTGA
     SEQ:022-3C12  (526)   GGGACTCAATACGAATTGA
SEQ:023-3N19(G2)   (526)   GGGACTGAATACAAATTGA
     SEQ:024-G2.2  (526)   GGGACTCAATACGAATTGA
      SEQ:025-2C3  (526)   GGGCCACAATACGAATTGA
     SEQ:026-2F11  (526)   AGGCCTAAATACGAATTGA
SEQ:027-KV11(6C7)  (526)   GGGCCTAAATACAAATTGA
SEQ:028-KV6(3A1)   (526)   GGGCCTAAATACAAATTGA
SEQ:029-KV2(2D1)   (526)   GGGCCAAAATACAAATTGA
     SEQ:030-N2.5  (526)   GGGCCACAATACAAATTGA
SEQ:031-KV5(2H6)   (526)   GGGCCTGAATACAAATTGA
      SEQ:032-3E5  (526)   GGGCCTCAATACGAATTGA
      SEQ:033-G2.1 (526)   GGGACTCAATACGAATTGA
SEQ:034-3H24(G2)   (526)   GGGACTCAATACGAATTGA
SEQ:035-KV10(4G6)  (526)   GGGCCACAATACAAATTGA
SEQ:036-KV12(6D4)  (526)   AGGCCACAATACAAATTGA
     SEQ:037-N2.2  (526)   AGGCCACAATACAAATTGA
     SEQ:038-N2.3  (526)   AGGCCACAATACAAATTGA
     SEQ:039-N2.1  (526)   AGGCCACAATACAAATTGA
SEQ:040-KV4(2E12)  (526)   GGGCCACAATACAAATTGA
SEQ:041-KV9(4C6)   (526)   GGGCCACAATACGAATTGA
      SEQ:042-7D6  (526)   GGGATTAAATACGAATTGA
      SEQ:043-3F3  (526)   GGGCCAGAATACGAATTGA
SEQ:044-2D11(G2)   (526)   AGGCCAGAATACGAATTGA
SEQ:045-3C23(G2)   (526)   GGGCCACAATACGAATTGA
      SEQ:046-G2.3 (526)   GGGCCAGAATACGAATTGA
      SEQ:047-2A3  (526)   AGGCCTAAATACAAATTGA
      SEQ:048-2F4  (526)   AGGCCAGAATACGAATTGA
SEQ:049-2B9(G2)    (526)   AGGCCAAAATACGAATTGA
     SEQ:050-2C5   (526)   AGGCCAAAATACGAATTGA
SEQ:051-KV1(2A6)   (526)   GGGCCAGAATACGAATTGA
SEQ:052-2D13(G2)   (526)   AGGCCAAAATACGAATTGA
     SEQ:053-3C8   (526)   GGGCCAAAATACAAATTGA
     SEQ:054-2D5   (526)   AGGACAAAATACAAATTGA
```

Figure 4 h

(Signal peptide)   (Mature region)

```
                        -35                                -1 1                                      40
SEQ:055-405(pumilus)  (1) --MKFVKRRIIALVTILVLSVTSLFAMQP-SAKAA|EHNPVVMVHGIGGASYNFAGIKSYLVSQGWSRGKLYAVDF
SEQ:056-406(subtilis) (1) --MKFVKRRIIALVTILMLSVTSLFALQP-SAKAA|EHNPVVMVHGIGGASFNFAGIKSYLVSQGWSRDKLYAVDF
SEQ:057-402(megat.)   (1) --MKFVKRRIIALVTILVLSVTSLFAMQP-SAKAA|DTIQLLWFTGIGGASYNFAGIKSYLVSQGWSRGKLYAVDF
SEQ:058-400(lentus)   (1) --MKFVKRRIIALVTILVLSVTSLFAMQP-SAKAA|EHNPVVMVHGIGGASYNFAGIKSYLVSQGWSRGKLYAVDF
SEQ:059-396(circul.)  (1) --MKFIKRRIIALVTILVLSVTSLFAMQP-SAKAA|EHNPVVMVHGIGGASYNFAGIKSYLVSQGWSRGKLYAVDF
SEQ:060-392(azotof.)  (1) --MKFVKRRIIALVTILVLSVTSLFAMQP-SAKAA|EHNPVVMVHGIGGASYNFAGIKSYLVSQGWSRGELYAVDF
SEQ:061-398(firmus)   (1) --MKFVKRRIIALVTILVLSVTSLFAMQP-SAKAA|EHNPVVMVHGIGGASYNFAGIKSYLVSQGWSRGKLYAVDF
SEQ:062-393(badius)   (1) --MKFVKRRIIALVTILVLSVTSLFAMQP-SAKAA|EHNPVVMVHGIGGASYNFAGIKSYLVSQGWSRGKLYAVDF
SEQ:063-Dc5h          (1) --MKFVKRRIIALVTILMLSVTSLFALQP-SAKAA|EHNPVVMVHGIGGASYNFAGIKSYLVSQGWSRDKLYAVDF
SEQ:064-Dc5f          (1) --MKFVKRRIIALVTILMLSVTSLFALQP-SAKAA|EHNPVVMVHGIGGASFNFAGIKSYLVSQGWSRDKLYAVDF
SEQ:065-Dc5c1         (1) MKVIFVKKRSLQILVALALVLGSIAFIQPKEAKAA|EHNPVVMVHGMGGASYNFASIKRYLVSQGWDQNQLFAIDF
SEQ:066-Dc5a2         (1) MKVIFVKKRSLQILVVLALVMGSMAFIQPKEIRAA|EHNPVVMVHGMGGASYNFASIKSYLVSQGWDRNQLFAIDF
SEQ:067-Dc512         (1) MKVIFVKKRSLQILIALALVIGSMAFIQPKEAKAA|EHNPVVMVHGIGGASYNFFSIKSYLATQGWDRNQLYAIDF
SEQ:068-Sga           (1) --MKFVKRRIIALVTILMLSVTSLFALQP-SAKAA|EHNPVVMVHGIGGASFNFAGIKSYLVSQGWSRDKLYAVDF
SEQ:069-Sgc           (1) --MKFVKRRIIALVTILMLSVTSLFALQP-SAKAA|EHNPVVMVHGIGGASFNFAGIKSYLVSQGWSRDKLYAVDF
SEQ:070-Sgd           (1) --MKFVKRRIIALVTILMLSVTSLFALQP-SAKAA|EHNPVVMVHGIGGASFNFAGIKSYLVSQGWSRDKLYAVDF
SEQ:071-Sgf           (1) --MKFVKRRIIALVTILMLSVTSLFALQP-SAKAA|EHNPVVMVHGIGGASFNFAGIKSYLVSQGWSRDKLYAVDF
SEQ:072-Sgh           (1) --MKFVKRRIIALVTILMLSVTSLFALQP-SAKAA|EHNPVVMVHGIGGASYNFASIKSYLVNQGWDRNQLFAIDF
SEQ:073-Mt2b1         (1) MKVIFVKKRSLQILVALALVIGSMAFIQPKEIKAA|EHNPVVMVHGIGGASYNFASIKSYLVNQGWDRNQLFAIDF
SEQ:074-H2a           (1) --MKFVKRRIIALVTILMLSVTSLFALQP-SAKAA|EHNPVVMVHGIGGASFNFAGIKSYLVSQGWSRDKLYAVDF
```

Figure 5a

EP 0 995 060

```
                          41                                                                      115
SEQ:055-405(pumilus)  (73) WDKTGTNYNNGPVLSRFVQKVLDETGAKKVDIVAHSMGGANTPYYIKNLDGGNKIENVVTLGGANRSTTSKALPG
SEQ:056-406(subtilis) (73) WDKTGTNYNNGPVLPRFVQKVLDETGAKKVDIVAHSMGGANTLYYIKNLDGGNKVANVVTLGGANRLTTGKALPG
SEQ:057-402(megat.)   (73) WDKTGTNYNNGPVLSRFVQKVLDETGAKKVDIVAHSMGGANTLYYIKNLDGGNKIENVVTLGGANRLTTSKALPG
SEQ:058-400(lentus)   (73) WDKTGTNYNNGPVLSRFVQKVLDETGAKKVDIVAHSMGGANTLYYIKNLDGGNKIENVVTLGGANRLTTSKALPG
SEQ:059-396(circul.)  (73) WDKTGTNYNNGPVLSRFVQKVLDETGAKKVDIVAHSMGGANTLYYIKNLDGGNKIENVVTLGGANRLTTSKALPG
SEQ:060-392(azotof.)  (73) WDKTGTNYNNGPVLSRFVQKVLDETGAKKVDIVAHSMGGANTLYYIKNLDGGNKIENVVTLGGANRLTTSKALPG
SEQ:061-398(firmus)   (73) WDKTGTNYNNGPVLSRFVQKVLDETGAKKVDIVAHSMGGANTLYYIKNLDGGNKIENVVTLGGANRLTTSKALPG
SEQ:062-393(badius)   (73) WDKTGTNYNNGPVLSRFVQKVLDETGAKKVDIVAHSMGGANTLYYIKNLDGGNKIENVVTLGGANRLTTSKALPG
SEQ:063-Dc5h          (73) KDKTGTNYNNGPVLSRFVQKVLDETGAKKVDIVAHSMGGANTLYYIKNLDGGNKVENVVTLGGANRLTTGKALPG
SEQ:064-Dc5f          (73) XDKTGNNRNNGPRLSRFVKDVLDKTGAKKVDIVAHSMGGANTLYYIKNLDGGDKIENVVTLGGANGLVSLRALPG
SEQ:065-Dc5c1         (76) IDKTGNNLNNGPRLSRFVKDVLAKTGAKKVDIVAHSMGGANTLYYIKNLDGGDKIENVVTIGGANGLVSLRALPG
SEQ:066-Dc5a2         (76) IDKTGNNRNNGPRLSRFVKDVLAKTGAKKVDIVAHSMGGANTLYYIKNLDGGDKIENVVTLGGANGLVSLRALPG
SEQ:067-Dc512         (76) IDKTGNNRNNGPRLSRFVKDVLDKTGAKKVDIVAHSMGGANTLYYIKNLDGGDKIENVVTIGGANGLVSSRALPG
SEQ:068-Sga           (73) RDKTGNNLNNGPVLSRFVKKVLDETGAKKVDIVAHSMGGANTLYYIKNLDGGNKIENVVTLGGANRLVTGKALPG
SEQ:069-Sgc           (73) WDKTGNNLNNGPVLSRFVKKVLDETGAKKVDIVAHSMGGANTLYYIKNLDGGNKIENVVTLGGANRLVTGKALPG
SEQ:070-Sgd           (73) SDKTGNNLNNGPVLSRFVKKVLDETGAKKVDIVAHSMGGANTLYYIKNLDGGNKIENVVTLGGANRLVTGKALPG
SEQ:071-Sgf           (73) KDKTGNNRNNGPRLSRFVKDVLDKTGAKKVDIVAHSMGGANTLYYIKNLDGGDKIENVVTLGGANGLVSSRALPG
SEQ:072-Sgh           (73) IDKTGNNRNNGPRLSRFVKDVLDKTGAKKVDIVAHSMGGANTLYYIKNLDGGDKIENVVTIGGANGLVSSRALPG
SEQ:073-Mt2b1         (76) IDKTGNNRNNGPRLSRFVKDVLDKTGAKKVDIVAHSMGGANTLYYIKNLDGGDKIENVVTIGGANGLVSLRALPG
SEQ:074-H2a           (73) RDKTGNNRNNGPRLSKFVKDVLDKTGAKKVDIVAHSMGGANTLYYIKNLDGGDKIENVVTIGGANGLVSSRALPG
```
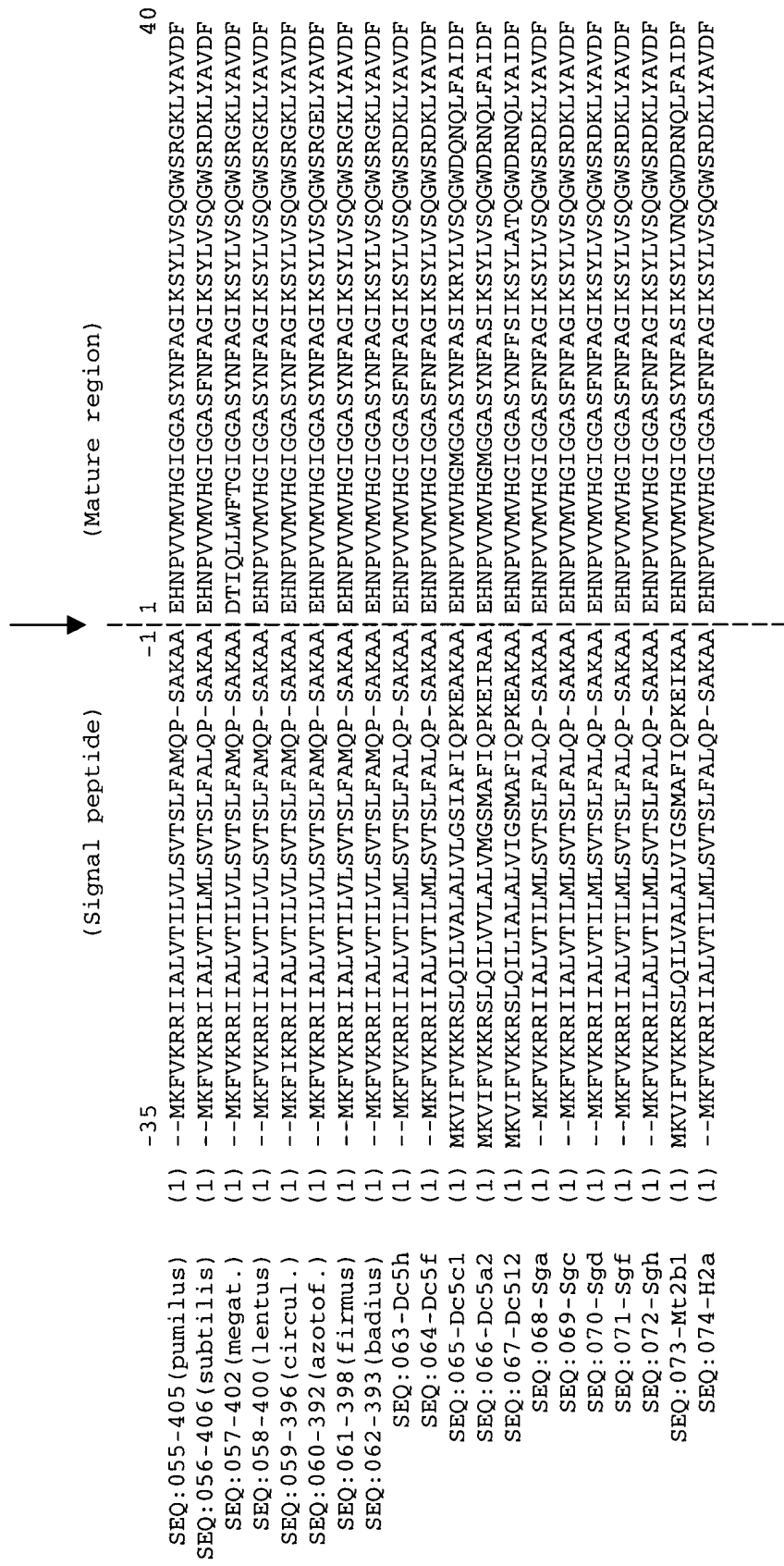
Figure 5b.

```
                                       116                                                                        181
SEQ:055-405(pumilus)  (148) TDPNQKILYTSIYSSADMIVMN-YLSKLDGAKNAQIHGVGHIGLLMNSQVNSLIKEGLNGGGQNTN
SEQ:056-406(subtilis) (148) TDPNQKILYTSIYSSADMIVIN-YLSRLDGARNVQIHGVGHIGLLMNSQVNSLIKEGLNGGGLNTN
SEQ:057-402(megat.)   (148) TDPNQKILYTSIYSSADMIVMN-YLSKLDGAKNVQIHGVGHIGLLMNSQVNSLIKEGLNGGGHNTN
SEQ:058-400(lentus)   (148) TDPNQKILYTSIYSSADMIVMN-YLSKLDGAKNVQIHGVGHIGLLMNSQVNSLIKEGLNGGGLNTN
SEQ:059-396(circul.)  (148) TDPNQKILYTSIYSSADMIVMN-YLSKLDGAKNVQIHGVGHIGLLMNSQVNSLIKEGLNGGGLNTN
SEQ:060-392(azotof.)  (148) TDPNQKILYTSIYSSANMIVMN-YLSKLDGAKNVQIHGVGHIGLLMNSQVNSLIKEGLNGGGLDTN
SEQ:061-398(firmus)   (148) TDPNQKILYTSIYSSADMIVMN-YLSKLDGAKNAQIHGVGHIGLLMNSQVNSLIKEGLNGGGHNTN
SEQ:062-393(badius)   (148) TDPNQKILYTSIYSSADMIVMN-YLSRLDGARNVQIHGVGHIGLLMNSQVNSLIKEGLNGGGHNTN
SEQ:063-Dc5h          (148) TDPNQKILYTSIYSSADMIVMN-YLSRLDGARNVQIHGVGHIGLLYSSQVNSLIKEGLNGGGLNTN
SEQ:064-Dc5f          (148) TDPNQKILYTSVYSSADLIVVN-SLSRLIGARNLIHGVGHIGLLTSSQVKGYIKEGLNGGGLNTN
SEQ:065-Dc5c1         (151) TDPNQKILYTSVYSSADLIVVN-SLSRLIGARNVLIHGVGHIGLLTSSQVKGYIKEGLNGGGLNTN
SEQ:066-Dc5a2         (151) TDPNQKILYTSVYSSADLIVVN-SLSRLIGARNVLIHGVGHIGLLASSQVKGYIKEGLNGGGQNTN
SEQ:067-Dc512         (151) TDPNQKILYTSVYSSADLIVVN-SLSQFNWRKKHPDPGVGHIGLLTSSQVKGYIKEGLNGGGLNTN
SEQ:068-Sga           (148) TDPNQKILYTSVYSSADMIVMN-YLTKLDGAKNVQIHGVGHIGLLYSSQVNSLIKEGLNGGGLNTN
SEQ:069-Sgc           (148) TDPNQKILYTSVYSSADMIVMN-YLSKLDGAKNVQIHGVGHIGLLYSSQVNSLIKEGLNGGGLNTN
SEQ:070-Sgd           (148) TDPNQKILYTSVYSSADMIVMN-YLSKLDGAKNVQIHGVGHIGLLYSSQVNSLIKEGLNGGGLNTN
SEQ:071-Sgf           (148) TDPNQKILYTSVYSSADLIVVN-SLSRLIGARNVQIHGVGHIGLLTSSQVKGYIKEGLNGGGLNTN
SEQ:072-Sgh           (148) TDPNQKILYTSVYSSADLIVVN-SLSRLIGARNVQIHGVGHIGLLTSSLVKGYIKEGLNGGGQNTN
SEQ:073-Mt2b1         (151) TDPNQKILYTSVYKLSRSHCRQQSLSFNWLQETVQIHGVGHIGLLTSSQVKGYIKEGLNGGGLNTN
SEQ:074-H2a           (148) TDPNQKILYTSVYKLSRSHCRQQSLSFNWLQETVQIHGVGHIGLLTSSQVKGYIKEGLNGGGLNTN
```

Figure 5c

```
                                  1                                                                           75
SEQ:075-1f15(G2)   (1)  EHNPVVMVHGIGGASFNFAGIKSYLVSQGWSRGKLYAVDFWDKTGTNYNNGPVLSRFVKKVLDETGAKKVDIVAH
     SEQ:076-3C12  (1)  EHNPVVMVHGIGGASFNFAGIKSYLVSQGWSRGKLYAVDFWDKTGTNYNNGPVLSRFVKKVLDETGAKKVDIVAH
SEQ:077-3N19(G2)   (1)  EHNPVVMVHGIGGASFNFAGIKSYLVSQGWSRGKLYAVDFWDKTGTNYNNGPVLSRFVKDVLDKTGAKKVDIVAH
   SEQ:078-G2.2    (1)  EHNPVVMVHGIGGASFNFAGIKSYLVSQGWSRGKLYAVDFWDKTGTNYNNGPVLSRFVKKVLDKTGAKKVDIVAH
     SEQ:079-2C3   (1)  EHNPVVMVHGIGGASFNFAGIKSYLVSQGWSRGKLYAVDFWDKTGTNYNNGPVLSRFVKKVLDETGAKKVDIVAH
     SEQ:080-2F11  (1)  EHNPVVMVHGIGGASYNFAGIKSYLVSQGWSRGKLYAVDFWDKTGTNYNNGPVLSRFVKKVLDETGAKKVDIVAH
SEQ:081-KV11(6C7)  (1)  EHNPVVMVHGIGGASFSFAGIKSYLVSQGWSRGKLYPVDFWDKTGTNYNNGPVLSRFVKKVLDETGAKKVDIVAH
SEQ:082-KV6(3A1)   (1)  EHNPVVMVHGIGGASFSFAGIKSYLVSQGWSRGKLYAVDFWDKTGTNYNNGPVLSRFVQKVLDETGAKKVDIVAH
SEQ:083-KV2(2D1)   (1)  EHNPVVMVHGIGGASYSFAGIKSYLVSQGWSRGKLYAVDFWDKTGTNYNNGPVLSRFVQKVLDETGAKKVDIVAH
   SEQ:084-N2.5    (1)  EHNPVVMVHGIGGASYSFAGIKSYLVSQGWSRGKLYAVDFWDKTGTNYNNGPVLSRFVQKVLDETGAKKVDIVAH
SEQ:085-KV5(2H6)   (1)  EHNPVVMVHGIGGASYNFAGIKSYLVSQGWSRGKLYAVDFWDKTGTNYNNGPVLSRFVQKVLDETGAKKVDIVAH
     SEQ:086-3E5   (1)  EHNPVVMVHGIGGASFNFAGIRSYLVSQGWSRGKLYTVDFWDKTGTNYNNGPVLSRFVQKVLDETGAKKVDIVAH
   SEQ:087-G2.1    (1)  EHNPVVMVHGIGGASFNFAGIRSYLVSQGWSRGKLYAVDFWDKTGTNYNNGPVLSRFVQKVLDETGAKKVDIVAH
SEQ:088-3H24(G2)   (1)  EHNPVVMVHGIGGASFNFAGIKSYLVSQGWSRGKLYAVDFWDKTGTNYNNGPVLSRFVQKVLDETGAKKVDIVAH
SEQ:089-KV10(4G6)  (1)  EHNPVVMVHGIGGASFNFAGIKSYLVSQGWPRDKLYAVDFWDKTGTNYNNGPVLSRFVQKVLDETGAKKVDIVAH
SEQ:090-KV12(6D4)  (1)  EHNPVVMVHGIGGASFSFAGIKSYLVSQGWPRDKLYAVDFWDKTGTNYNNGPVLSRFVQKVLDETGAKKVDIVAH
   SEQ:091-N2.2    (1)  EHNPVVMVHGIGGASFSFAGIRSYLVSQGWPRDKLYAVDFWDKTGTNYNNGPVLSRFVQKVLDETGAKKVDIVAY
   SEQ:092-N2.3    (1)  EHNPVVMVHGIGGASFSFAGIRSYLVSQGWPRDKLYAVDFWDRTGTNYNNGPVLSRFVQKVLDETGAKKVDIVAH
   SEQ:093-N2.1    (1)  EHNPVVMVHGIGGASFNFAGIRSYLVSQGWSRGKLYAVDFWDRTGTNYNNGPVLSRFVQKVLDETGAKKVDIVAH
SEQ:094-KV4(2E12)  (1)  EHNPVVMVHGIGGTSFNFAGIKSYLVSQGWSRGKLYAVDFSDKTGTNYNNGPVLSRFVQKVLDETGAKKVDIVAH
SEQ:095-KV9(4C6)   (1)  EHNPVVMVHGIGGASFSFAGIKSYLVSQGWSRDKLYAVDFKDKTGTNYNNGPVLSRFVKKVLDETGAKKVDIVAH
     SEQ:096-7D6   (1)  KHNPVVMVHGIGGASFNFAGIKSYLVSQGWSRDKLYAVDFWGKTGTNYNNGPVLSRFVKKVLDETGAKKVDIVAH
     SEQ:097-3F3   (1)  EHNPVVMVHGIGGASYNFAGIKSYLESQGWSRGKLYAVDFWDKTGTNYNNGPVLSRFVQKALDETGAKKVDIVAH
SEQ:098-2D11(G2)   (1)  EHNPVVMVHGIGGASFNFAGIKSYLVSQGWSRGKLYAVDFWDKTGTNYNNGPVLSRFVKKVLDETGAKKVDIVAH
SEQ:099-3C23(G2)   (1)  EHNPVVMVHGIGGASFNFAGIKSYLVSQGWSRGKLYAVDFWDRTGTNYNNGPVLSRFVQKVLDETGAKKVDIVAH
   SEQ:100-G2.3    (1)  EHNPVVMVHGIGGASFNFAGIKSYLVSQGWSRGKLYAVDFWDRTGTNYNNGPVLSRFVQKVLDETGAKKVDIVAH
     SEQ:101-2A3   (1)  EHNPVVMVHGIGGASFNFAGIKSYLVSQGWSRGKLYAVDFWDKTGTNYNNGPVLSRFVQKVLDETGAKKVDIVAH
     SEQ:102-2F4   (1)  EHNPVVMVHGIGGASFNFAGIKSYLVSQGWSRDKLYAVDFKDKTGTNYNNGPVLSRFVKKVLDETGAKKVDIVAH
SEQ:103-2B9(G2)    (1)  EHNPVVMVHGIGGASFNFAGIKSYLVSQGWSRDKLYAVDFWDKTGTNYNNGPVLSRFVKKVLDETGAKKVDIVAH
     SEQ:104-2C5   (1)  EHNPVVMVHGIGGASFNFAGIKSYLVSQGWSRGKLYAVDFWDKTGTNYNNGPVLSRFVKKVLDETGAKKVDIVAH
SEQ:105-KV1(2A6)   (1)  KHNPVVMVHGIGGASFNFAGIKSYLVSQGWSRGKLYAVDFKDKTGTNYNNGPVLSRFVQKVLDETGAKKVDIVAH
SEQ:106-2D13(G2)   (1)  EHNPVVMVHGIGGASFNFAGIKSYLVSQGWSRDELYAVDFWDETGTNYNNGPVLSRFVQKVLDETGAKKVDIVAH
     SEQ:107-3C8   (1)  EHNPVVMVHGIGGASFNFAGIKSYLVSQGWSRDKLYAVDFWDKTGTNYNNGPVLSRFVKKVLDETGAKKVDIVAH
     SEQ:108-2D5   (1)  EHNPVVMVHGIGGASFNFAGIKSYLVSQGWSRGKLYAVDFWDKTGTNYNNGPVLSRFVQKVLDETGAKKVDIVAH
```

Figure 6a

```
                                76                                                              150

SEQ:075-1f15(G2)   (76)  SMGGANTLYYIKNLDGGNKVENVVTLGGTNRSTTSKALPGTDPNQKILYTSIYSSADMIVMNYLSKLDGAKNVQI
SEQ:076-3C12       (76)  SMGGANTLYYIKNLDGGNKIENVVTLGGANRSTTSKALPGTDPNQKILYTSIYGSADMIVMNYLSKLDGAKNVQI
SEQ:077-3N19(G2)   (76)  SMGGANTLYYIKNLDGGNKIENVVTLGGANRLTTSKALPGTDPNQKILYTSIYGSADMIVMNYLSKLDGAKNVQI
SEQ:078-G2.2       (76)  SMGGANTLYYIKNLDGGNKIENVVTLGGANRLTTSKALPGTDPNQKILYTSIYGSADMIVMNYLSKLDGAKNVQI
SEQ:079-2C3        (76)  SMGGANTLYYIKNLDGGNKIENVVTIGGANGLVSSRALPGTDPNQKILYTSVYSSADLIVVNSLSRLIGARNVQI
SEQ:080-2F11       (76)  SMGGANTLYYIKNLDGGNKIENVVTLGGANRLTTSRALPGTDPNQKILYTSIYSSADMIVMNYLSKLDGAKNVQI
SEQ:081-KV11(6C7)  (76)  SMGGANTLYYIKNLDGGNKIENVVTLGGANRLTTSKALPGTDPNQKILYTSVYSSADMIVMNYLSKLDGAKNVQI
SEQ:082-KV6(3A1)   (76)  SMGGANTLYYIKNLDGGNKIENVVTLGGANRLTTSKALPGTDPNQKILYTSVYSSADMIVMNYLSKLDGAKNVQI
SEQ:083-KV2(2D1)   (76)  SMGGANTLYYIKNLDGGNKIENVVTLGGANRLTTSKALPGTDPNQKILYTSVYSSADMIVMNYLSKLDGAKNVQI
SEQ:084-N2.5       (76)  SMGGANTLYYIKNLDGGNKIENVVTLGGANRLTTSKALPGTDPNQKILYTSIYSSADMIVMNYLSKLDGAKNVQI
SEQ:085-KV5(2H6)   (76)  SMGGANTLYYIKNLDGGNKIENVVTLGGANRLTTSKALPGTDPNQKILYASVYSSADMIVMNYLSKLDGAKNVQI
SEQ:086-3E5        (76)  SMGGANTLYYIKNLDGGNKIENVVTLGGANRLTTSRALPGTDPNQKILYTSIYSSADMIVMNYLSKLDGAKNVQI
SEQ:087-G2.1       (76)  SMGGANTLYYIKNLDGGNKIENVVTLGGTNRLTTSRALPGTDPNQKILYTSIYSSADMIVMNYLSKLDGAKNVQI
SEQ:088-3H24(G2)   (76)  SMGGANTLYYIKNLDGGNKVENVVTLGGANRLTTSKALPGTDPNQKILYTSIYSSADMIVMNYLSKLDGAKNVQI
SEQ:089-KV10(4G6)  (76)  SMGGANTLYYIKNLDGGNKVESVVTLGGANRLTTSKALPGTDPNQKILYTSIYSSADMIVMNYLSKLDGAKNVQI
SEQ:090-KV12(6D4)  (76)  SMGGANTLYYIKNLDGGNKVENVVTLGGANRLTTSKALPGTDPNQKILYTSVYSSADMIVMNYLSKLDGAKNVQI
SEQ:091-N2.2       (76)  SMGGANTLYYIKNLDGGNKVGNVVTLGGANRLTTGKALPGTDPNQKILYTSVYSSADMIVMNYLSKLDGAKNVQI
SEQ:092-N2.3       (76)  SMGGANTLYYIKNLDGGNKVENVVTLGGANRLTTGKALPGTDPNQKILYTSVYSSADMIVMNYLSKLDGAKNVQI
SEQ:093-N2.1       (76)  SMGGANTLYYIKNLDGGNKVENVVTLGGANRLTTGKALPGTDPNQKILYTSVYSSADMIVMNYLSKLDGAKNVQI
SEQ:094-KV4(2E12)  (76)  SMGGANTLYYIKNLDGGNKIENVVTLGGANRLTTSKALPGTDPNQKILYTSIYSSADMIVMNYLSKLDGAKNVQI
SEQ:095-KV9(4C6)   (76)  SMGGANTLYYIKNLDGGNKVENVVTLGGANRLTTSKALPGTDPNQKILYTSIYSSADMVVMNYLSKLDGAKNVQI
SEQ:096-7D6        (76)  SMGGANTLYYIKNLDGGNKIENVVTLGGANRLTTSKALPGTDPNQKILYTSIYSSADMIVMNYLSKLDGAKNVQI
SEQ:097-3F3        (76)  SMGGANTLYYIKNLDGGNKIENVVTLGGANRSTTSKALPGTDPNQKILYTSIYSSADMIVMNYLSKLDGAKNVQI
SEQ:098-2D11(G2)   (76)  SMGGANTLYYIKNLDGGNKIENVVTLGGANRSTTSKALPGTDPNQKILYTSIYSSADMIVMNYLSKLDGAKNVQI
SEQ:099-3C23(G2)   (76)  SMGGANTLYYIKNLDGGNKIENVVTLGGANRSTTSKALPGTDPNQKILYTSIYSSADMIVMNYLSKLDGAKNVQI
SEQ:100-G2.3       (76)  SMGGANTLYYIKNLDGGNKIENVVTLGGANRSTTSKALPGTDPNQKILYTSIYSSADMIVMNYLSKLDGAKNVQI
SEQ:101-2A3        (76)  SMGGANTLYYIKNLDGGDKIENVVTLGGANRSTTSKALPGTDPNQKILYTSIYSSADMIVMNCLSKLDGAKNVQI
SEQ:102-2F4        (76)  SMGGANTLYYIKNLDGGNKIENVVTLGGANRSTTSKALPGTDPNQKILYTSIYSSADMIVMNYLSKLDGAKNVQI
SEQ:103-2B9(G2)    (76)  SMGGANTLYYIKNLDGGNKIENVVTLGGANRSTTSKALPGTDPNQKILYTSIYSSADMIVMNYLSKLDGAKNVQI
SEQ:104-2C5        (76)  SMGGANTLYYIKNLDGGNKIENVVTLGGANRSTTSKALPGTDPNQKILYTSIYSSADMIVMNYLSKLDGAKNVQI
SEQ:105-KV1(2A6)   (76)  SMGGANTLYYIKNLDGGNKIENVVTLGGANRSTTSKALPGTDPNQKILYTSIYSSADMIVMNYLSKLDGAKNVQI
SEQ:106-2D13(G2)   (76)  SMGGANTLYYIKNLDGGNKIENVVTLGGANRSTTSKALPGTDPNQKILYTSIYSSADMIVMNYLSKLDGAKNVQI
SEQ:107-3C8        (76)  SMGGANTLYYIKNLDGGNKIENVVTLGGANRSTTSKALPGTDPNQKILYTSIYSSADMIVMNYLSKLDGAKNVQI
SEQ:108-2D5        (76)  SMGGANTLYYIKNLDGGNKIENVVTLGGANRSTTSKALPGTDPNQKILYTSIYSSADMIVMNYLSKLDGAKNVQI
```

Figure 6b

```
                                  151                              180
SEQ:075-1f15(G2)     (151)  HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN
SEQ:076-3C12         (151)  HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN
SEQ:077-3N19(G2)     (151)  HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN
SEQ:078-G2.2         (151)  HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN
   SEQ:079-2C3       (151)  HGVGHIGLLTSSQVKGYIKEGLNGGGHNTN
SEQ:080-2F11         (151)  HGVGHIGLLMNSQVKGYIKEGLNGGGLNTN
SEQ:081-KV11(6C7)    (151)  HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN
SEQ:082-KV6(3A1)     (151)  HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN
SEQ:083-KV2(2D1)     (151)  HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN
   SEQ:084-N2.5      (151)  HGVGHIGLLYSSQVNSLIKEGLNGGGQNTN
SEQ:085-KV5(2H6)     (151)  HGVGHTGLLMNSQVNSLIKEGLNGGGHNTN
   SEQ:086-3E5       (151)  HGVGHIGLLYSSQVNSLIKEGLNGGGLNTN
   SEQ:087-G2.1      (151)  HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN
SEQ:088-3H24(G2)     (151)  HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN
SEQ:089-KV10(4G6)    (151)  HGVGHIGLLMNSQVNRLIKEGLNGGGHNTN
SEQ:090-KV12(6D4)    (151)  HGVGHIGLLMNSQVNRLIKEGLNGGGHNTN
   SEQ:091-N2.2      (151)  HGVGHIGLLMNSQVNRLIKEGLNGGGHNTN
   SEQ:092-N2.3      (151)  HGVGHIGLLMNSQVNRLIKEGLNGGGHNTN
   SEQ:093-N2.1      (151)  HGVGHIGLLMNSQVNSLIKEGLNGGGHNTN
SEQ:094-KV4(2E12)    (151)  HGVGHIGLLMNSQVNSLIKEGLNGGGHNTN
SEQ:095-KV9(4C6)     (151)  HGVGHIGLLMNSQVNSLIKEGLNGGGHNTN
   SEQ:096-7D6       (151)  HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN
   SEQ:097-3F3       (151)  HGVGHIGLLMNSQVNSLIKEGLNGGGQNTN
SEQ:098-2D11(G2)     (151)  HGVGHIGLLMNSQVNSLIKEGLNGGGQNTN
SEQ:099-3C23(G2)     (151)  HGVGHIGLLMNSQVNSLIKEGLNGGGHNTN
SEQ:100-G2.3         (151)  HGVGHIGLLMNSQVNSLIKEGLNGGGQNTN
   SEQ:101-2A3       (151)  HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN
   SEQ:102-2F4       (151)  HGVGHIGLLMNSQVNSLIKEGLNGGGQNTN
SEQ:103-2B9(G2)      (151)  HGVGHIGLLMNSQVNSLIKEGLNGGGQNTN
   SEQ:104-2C5       (151)  HGVGHIGLLMNSQVNSLIKEGLNGGGQNTN
SEQ:105-KV1(2A6)     (151)  HGVGHIGLLMNSQVNSLIKEGLNGGGQNTN
SEQ:106-2D13(G2)     (151)  HGVGHIGLLMNSQVNSLIKEGLNGGGQNTN
   SEQ:107-3C8       (151)  HGVGHIGLLMNSQVNSLIKEGLNGGGQNTN
   SEQ:108-2D5       (151)  HGVGHIGLLMNSQVNSLIKEGLNGGGQNTN
```

Figure 6c